

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE  
(Case No. 99-372-F1)**

<b>In re Application of: Welcher et al.</b>	)	
	)	
<b>Serial No.: 11/200,389</b>	)	<b>Before the Examiner: J. Seharaseyon</b>
	)	
<b>Filed: August 8, 2005</b>	)	<b>Group Art Unit: 1647</b>
	)	
<b>For: Interferon-like Molecules and Uses Thereof</b>	)	<b>Confirmation No.: 3469</b>
	)	

Mail Stop Amendment  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Sir:

**RESPONSE TO OFFICE ACTION MAILED NOVEMBER 23, 2007**

Responsive to the Office Action mailed November 23, 2007, Applicants respectfully request reconsideration of the above-identified application in view of the following amendments and remarks.

**Amendments to the Specification:** Pursuant to 37 C.F.R. § 1.121, Applicants present the amendments to the specification at page 2, marked up to show changes made relative to the immediate prior version of the specification.

**Amendments to the Claims:** Pursuant to 37 C.F.R. § 1.121, Applicants present a complete listing of the claims, including marked up versions of all currently amended claims, at pages 3-5

**Remarks:** Applicants' Remarks begin on page 6 of this paper.

**Amendments to the Specification under 37 C.F.R. § 1.121**

Please amend the specification at page 1, line 1 as follows:

**INTERFERON-LIKE ~~MOLECULES~~ PROTEINS AND USES THEREOF**

**Amendments to the Claims under 37 C.F.R. § 1.121**

Claim 1 (original): An isolated polypeptide comprising an amino acid sequence:

- (a) as set forth in SEQ ID NO: 5; or
- (b) encoded by the DNA insert in ATCC Deposit No. PTA-976.

Claim 2 (currently amended): An isolated polypeptide comprising:

- ~~(a) — an the amino acid sequence as set forth in SEQ ID NO: 6, optionally further comprising an amino-terminal methionine;~~
- ~~(b) — an amino acid sequence that is at least about 70 percent identical to the amino acid sequence set forth in SEQ ID NO: 5, wherein the polypeptide upon exposure to mammalian cells, causes an increase in cellular protein tyrosine phosphorylation; or~~
- ~~(c) — a fragment of the amino acid sequence set forth in SEQ ID NO: 5 comprising at least about 25 amino acid residues, wherein the polypeptide upon exposure to mammalian cells, causes an increase in cellular protein tyrosine phosphorylation, or is antigenic.~~

Claim 3 (cancelled).

Claim 4 (currently amended): An isolated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence:

- (a) as set forth in SEQ ID NO: 4;
  - (b) of the DNA insert in ATCC Deposit No. PTA-976; or
  - (c) encoding a polypeptide as set forth in SEQ ID NO: 5; ~~or~~
  - ~~(d) — that hybridizes to the complement of the nucleotide sequence of any of (a)-(c) under hybridization conditions allowing no more than a 21% mismatch between the nucleotide sequences;~~
- ~~wherein the encoded polypeptide upon exposure to mammalian cells, causes an increase in cellular protein tyrosine phosphorylation.~~

Claims 5-7 (cancelled).

Claim 8 (currently amended): A composition comprising the polypeptide of any of Claims 1, 2, or ~~3~~ 4, and a pharmaceutically acceptable formulation agent.

Claim 9 (original): The composition of Claim 8, wherein the pharmaceutically acceptable formulation agent is a carrier, adjuvant, solubilizer, stabilizer, or anti-oxidant.

Claim 10 (currently amended): The composition of Claim 8, wherein the polypeptide comprises ~~an~~ the amino acid sequence as set forth in SEQ ID NO: 6.

Claim 11 (currently amended): A polypeptide comprising a derivative of the polypeptide of any of Claims 1, 2, or ~~3~~ 4.

Claim 12 (original): The polypeptide of Claim 11 that is covalently modified with a water-soluble polymer.

Claim 13 (original): The polypeptide of Claim 12, wherein the water-soluble polymer is polyethylene glycol, monomethoxy-polyethylene glycol, dextran, cellulose, poly-(N-vinyl pyrrolidone) polyethylene glycol, propylene glycol homopolymers, polypropylene oxide/ethylene oxide copolymers, polyoxyethylated polyols, or polyvinyl alcohol.

Claim 14 (currently amended): A fusion polypeptide comprising the polypeptide of any of Claims 1, 2, or ~~3~~ 4 fused to a heterologous amino acid sequence.

Claim 15 (original): The fusion polypeptide of Claim 14, wherein the heterologous amino acid sequence is an IgG constant domain or fragment thereof.

Claim 16 (currently amended): A polypeptide produced by a process comprising culturing a host cell comprising a vector comprising a nucleic acid molecule comprising a nucleotide sequence:

(a) as set forth in SEQ ID NO: 4;  
(b) of the DNA insert in ATCC Deposit No. PTA-976; or  
(c) encoding a polypeptide as set forth in SEQ ID NO: 5; ~~or~~  
(d) ~~that hybridizes to the complement of the nucleotide sequence of any of (a)-(c)~~  
~~under hybridization conditions allowing no more than a 21% mismatch between the nucleotide~~  
~~sequences;~~  
~~wherein the polypeptide upon exposure to mammalian cells, causes an increase in cellular~~  
~~protein tyrosine phosphorylation;~~  
under suitable conditions to express the polypeptide, and optionally isolating the  
polypeptide from the culture.

Claims 17-18 (cancelled).

Claim 19 (currently amended):      The polypeptide of ~~any of Claim[[s]]~~ 16, ~~17, or~~ 18, wherein  
the host cell is a eukaryotic cell.

Claim 20 (currently amended):      The polypeptide of ~~any of Claim[[s]]~~ 16, ~~17, or~~ 18, wherein  
the host cell is a prokaryotic cell.

## **REMARKS**

Claims 2, 4, 8, 10, 11, 14, 16, 19, and 20, as amended, and claims 1, 9, 12, 13, and 15 are pending in the instant application. Claims 3, 5-7, 17, and 18 have been canceled without prejudice or disclaimer. No new matter has been added as a result of the above-described amendments. The rejections set forth in the Office Action have been overcome by amendment or are traversed by argument below.

### **1. Claim of priority**

The Office Action states that the instant application appears to claim subject matter disclosed in U.S. Application No. 09/927,850 (the '850 application), and that Applicants must amend the specification to insert a reference to the '850 application as the first sentence of the specification if Applicants intend to rely on the filing date of the '850 application under 35 U.S.C. §§ 119(e), 120, 121, or 365(c).

Coinciding with the submission of this Response, Applicants have submitted a Petition for an Unintentionally Delayed Domestic Priority Claim in order to amend the first sentence of the instant application to insert a reference to the '850 application.

### **2. Objections to the Specification**

The Office Action contains an objection to the specification because the title of the invention is not descriptive. The Action states that a new title is required that is clearly indicative of the invention to which the claims are directed.

Applicants have amended the title to read: "Interferon-Like Proteins and Uses Thereof," which Applicants contend is clearly indicative of the invention to which the claims are directed. Applicants, therefore, respectfully request that this ground of objection be withdrawn.

The Office Action asserts an objection to the specification because of the improper use of the trademark "Quick Spin" and "Taq polymerase," which the Action states should be capitalized and accompanied by generic terminology.

Applicants have searched the U.S. Patent and Trademark Office Trademark Electronic Search System (TESS), but have not found a record for the term "Quick Spin" with respect to

Qiagen's G-50 column. Applicants were also unable to find a record for the term "Taq polymerase." Applicants contend that because the terms "Quick Spin" and "Taq polymerase" do not appear to be registered trademarks, these terms do not to be capitalized or accompanied by generic terminology. Applicants respectfully request that this ground of objection be withdrawn.

**3. Rejection of claims 5, 6, and 16-20 under 35 U.S.C. § 112, second paragraph**

Claims 5, 6, and 16-20 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that applicants regard as the invention.

a. Hybridization conditions

Claims 5, 6, and 16-18 are rejected for reciting the term "hybridization conditions," which the Action states is insufficiently defined in the specification.

Applicants have cancelled claims 5, 6, 17, and 18, and have amended claim 16 to delete subpart (d). As claim 16 no longer recites hybridization conditions, Applicants respectfully request that this ground of rejection be withdrawn.

b. Polypeptide production

Claims 16-18 are rejected for being indefinite since it is unclear how the polynucleotide complements of claims 16(d), 17(c), and 18(b) can encode a polypeptide having the activity of the polypeptides disclosed in the specification.

Applicants have cancelled claims 17 and 18, and have amended claim 16 to delete subpart (d). As claim 16 no longer recites subpart (d), Applicants respectfully request that this ground of rejection be withdrawn.

c. IFN-L polypeptide

Claims 2, 5, and 17 are rejected as being vague and indefinite for the reciting the term "at least about."

Applicants have cancelled claims 5 and 17, and have amended claim 2 to delete subpart (b). As claim 2 no longer recites the term "about," Applicants respectfully request that this ground of rejection be withdrawn.

Applicants submit that the claims as amended are in condition for allowance and respectfully request that the rejections under 35 U.S.C. § 112, second paragraph, be withdrawn.

**4. Rejection of claims 1-20 under 35 U.S.C. § 112, first paragraph**

**a. Rejection of claims 1-20 under the enablement requirement of 35 U.S.C. § 112, first paragraph**

Claims 1-20 are rejected under 35 U.S.C. § 112, first paragraph, as not being enabled by the specification such that one of skill in the art could make and use the invention as claimed. The Action specifically asserts that all possible variants of SEQ ID NO: 5 are not enabled, and that the amount of experimentation required to determine these variants would be undue.

Applicants respectfully disagree with the Action's assertion that the claimed variants of SEQ ID NO: 5 are not enabled. Nevertheless, solely in an effort to expedite prosecution of the pending claims to allowance, Applicants have cancelled claims 5, 6, 17, and 18, and have deleted claims 2(b), 2(c), 4(d), and 16(d). As the pending claims no longer recite variants of SEQ ID NO: 5, Applicants respectfully request that this ground of rejection be withdrawn.

Applicants reserve the right to pursue claims directed to the cancelled or deleted subject matter in a timely filed continuation or divisional application, or alternatively, reintroduce the cancelled or deleted subject matter in the instant application at such time as the Office indicates that the pending claims are otherwise in condition for allowance.

The Action also asserts that phrases such as "an amino acid sequence" and "a nucleic acid molecule" in the claims read upon various variants and fragments. Applicants have cancelled claim 6 and 18, and have amended claims 2(a) and 10 to recite "the" rather than "a" or "an." Applicants, therefore, respectfully request that this ground of rejection be withdrawn.

The Action further asserts that Applicants' referral to the deposit of PTA-976 in the specification and in claims 1, 4, 5, 16 and 17 is an insufficient assurance that all of the conditions of 37 C.F.R §§ 1.801-1.809 have been met. The Action states that Applicants must submit a statement



by an attorney of record over his or her signature, stating that a deposit has been made under the terms of the Budapest Treaty and that all restrictions imposed by the depositor on the availability to the public of the deposited material will be irrevocably removed upon the granting of a patent. The Action further states that the instant specification must be amended to recite the date of the deposit and the complete name and address of the depository, and that the claims must be amended to recite the accession number.

Pursuant to the Examiner's request, Applicants' representative submits the following statement: Applicants deposited cDNA encoding human IFN-L polypeptide with the American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, VA 20110-2209. The deposit was accepted by the ATCC, an International Depository Authority, under the provisions of the Budapest Treaty, and the deposit was designated as PTA-976. A copy of the ATCC receipt for this deposit, showing the patent deposit designation (Accession No. PTA-976) and the date on which the deposit was received by the ATCC (November 23, 1999), is attached. Pursuant to 37 C.F.R. § 1.808(a)(2), the deposit was made under conditions that assure that all restrictions imposed by the depositors on the availability to the public of the deposited material would be irrevocably removed upon the granting of a patent relying on the deposited biological material. In making the deposit, Applicants acknowledged their responsibility, pursuant to 37 C.F.R. § 1.805, to provide a replacement or supplemental deposit if the depository possessing the deposit is unable to furnish samples thereof or is able to furnish samples thereof but the deposit has become contaminated or has lost its capability to function as described in the specification. With regard to the assertion that the date of the deposit and the complete name and address of the depository is not referred to in the body of the specification, Applicants respectfully direct the Examiner's attention to page 92, lines 25-28 of the specification as-filed, where Applicants disclose that a deposit of cDNA encoding human IFN-L polypeptide, subcloned into pSPORT1 (Gibco BRL) and transfected into *E. coli* strain DH10B, having Accession No. PTA-976, were made with the American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209 on November 23, 1999. With regard to the assertion that the accession number of the deposit is not referred to in the claims, Applicants respectfully direct the Examiner's attention to claims 1(b), 4(b), and 16(b), as originally filed. Applicants contend that all the requirements of 37 C.F.R. §§ 1.801-1.809 have been met. *In re*

*Lundak*, 225 U.S.P.Q. 90 (Fed. Cir. 1985). Withdrawal of this rejection is therefore respectfully solicited.

Applicants submit that the claims as amended are in condition for allowance, and respectfully request that the rejections under the enablement requirement of 35 U.S.C. § 112, first paragraph, be withdrawn.

b. Rejection of claims 1-20 under the written description requirement of 35 U.S.C. § 112, first paragraph

Claims 1-20 have been rejected as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. The Action asserts that the specification does not disclose all possible variants of nucleic acid molecules that hybridize to the complement of the claimed nucleotide sequences with more than 21% mismatch. The Action also asserts that specification has failed to disclose any other sequence contemplated in the instant claims including IFN-L fragments and other variants, and thus the skilled artisan cannot envision the detailed chemical structures of the claimed polypeptide sequences. Finally, the Action asserts that the species specifically disclosed are not representative of the genus because the genus is highly variant.

Applicants respectfully disagree with the Action's assertion that the specification does not contain an adequate written description of the claimed invention. Nevertheless, solely in an effort to expedite prosecution of the pending claims to allowance, Applicants have cancelled claims 5, 6, 17, and 18, and have deleted claims 2(b), 2(c), 4(d), and 16(d). As the pending claims no longer recite the variants described above, Applicants respectfully request that this ground of rejection be withdrawn.

Applicants reserve the right to pursue claims directed to the cancelled or deleted subject matter in a timely filed continuation or divisional application, or alternatively, reintroduce the cancelled or deleted subject matter in the instant application at such time as the Office indicates that the pending claims are otherwise in condition for allowance.

Applicants submit that the claims as amended are in condition for allowance, and respectfully request that the rejection under the written description requirement of 35 U.S.C. § 112, first paragraph, be withdrawn.

**5. Rejection of claims 1-20 under 35 U.S.C. § 102(e)**

The Office Action asserts a rejection of claims 1-20 under 35 U.S.C. § 102(e) as being anticipated by U.S. Patent No. 6,433,145 (the '145 patent).

Pursuant to 37 C.F.R. § 41.202, Applicants suggest that an interference be declared between the instant application and U.S. Patent No. 6,433,145 (the '145 patent). The '145 patent issued on August 13, 2002 from U.S. Application No. 09/487,792 (the '792 application), which was filed on January 20, 2000. The '792 application is a continuation-in-part of U.S. Application No. 09/358,587 and International Application No. PCT/US99/16424, both filed on July 21, 1999, and claims the benefit of U.S. Provisional Application No. 60/093,643, filed July 21, 1998.

Applicants believe claims 1 and 51 of the '145 patent interfere with claims 1 and 2 of the instant application. Claims 1 and 51 of the '145 patent read as follows:

1. An isolated protein comprising a polypeptide having an amino acid sequence selected from the group consisting of:
  - (a) amino acids 1 to 207 of SEQ ID NO:2;
  - (b) amino acids 7 to 207 of SEQ ID NO:2;
  - (c) amino acids 2 to 207 of SEQ ID NO:2; and
  - (d) amino acids 28 to 207 of SEQ ID NO:2.
  
51. An isolated protein comprising a polypeptide having an amino acid sequence selected from the group consisting of:
  - (a) the amino acid sequence of a fragment of amino acid residues 1 to 207 of SEQ ID NO:2, wherein the fragment has anti-viral activity;
  - (b) the amino acid sequence of a fragment of amino acid residues 1 to 207 of SEQ ID NO:2, wherein the fragment inhibits bone marrow proliferation;
  - (c) the amino acid sequence of a fragment of amino acid residues 1 to 207 of SEQ ID NO:2, wherein the fragment activates the Jak/Stat pathway; and
  - (d) the amino acid sequence of a fragment of amino acid residues 1 to 207 of SEQ ID NO:2, wherein the fragment binds an antibody that specifically binds a protein having the amino acid sequence of SEQ ID NO:2.

Claims 1 and 2 of the instant application read as follows:

1. An isolated polypeptide comprising an amino acid sequence:
  - (a) as set forth in SEQ ID NO: 5; or
  - (b) encoded by the DNA insert in ATCC Deposit No. PTA-976.
2. An isolated polypeptide comprising the amino acid sequence as set forth in SEQ ID NO: 6, optionally further comprising an amino-terminal methionine.

Applicants propose the following counts:

1. An isolated polypeptide comprising the amino acid sequence of amino acids 1 to 207 of SEQ ID NO:2 of U.S. Patent No. 6,433,145.
2. An isolated polypeptide comprising the amino acid sequence of a fragment of amino acid residues 1 to 207 of SEQ ID NO:2, wherein the fragment has anti-viral activity, inhibits bone marrow proliferation, activates the Jak/Stat pathway, or binds an antibody that specifically binds a protein having the amino acid sequence of SEQ ID NO:2.

A comparison between the proposed counts, claims 1(a) and 51 of the '145 patent, and claims 1(a) and 2 of the instant application is provided in the claim chart below:

<b>Count 1</b>	<b>Claim 1(a) of '145 patent</b>	<b>Claim 1(a) of the instant application</b>
An isolated polypeptide	An isolated protein comprising a polypeptide	An isolated polypeptide
comprising the amino acid sequence of amino acids 1 to 207 of SEQ ID NO:2. of U.S. Patent No. 6,433,145.	having an amino acid sequence [that is] amino acids 1 to 207 of SEQ ID NO:2[.]	comprising an amino acid sequence . . . as set forth in SEQ ID NO: 5 . . . .
<b>Count 2</b>	<b>Claim 51 of '145 patent</b>	<b>Claim 2 of the instant application</b>
An isolated polypeptide	An isolated protein comprising a polypeptide	An isolated polypeptide
comprising the amino acid	having an amino acid	comprising the amino acid

sequence of a fragment of amino acid residues 1 to 207 of SEQ ID NO:2,	sequence [that is] the amino acid sequence of a fragment of amino acid residues 1 to 207 of SEQ ID NO:2,	sequence as set forth in SEQ ID NO: 6 . . . .
wherein the fragment has anti-viral activity, inhibits bone marrow proliferation, activates the Jak/Stat pathway, or binds an antibody that specifically binds a protein having the amino acid sequence of SEQ ID NO:2.	wherein the fragment has anti-viral activity; . . . wherein the fragment inhibits bone marrow proliferation; . . . wherein the fragment activates the Jak/Stat pathway; [or] wherein the fragment binds an antibody that specifically binds a protein having the amino acid sequence of SEQ ID NO:2.	[While claim 2 does not expressly recite this limitation, the polypeptide recited in the claim, which is the mature form of the full-length IFN-L polypeptide, would inherently have such properties.]

The sequence alignment provided in Exhibit A indicates that the amino acid sequence of SEQ ID NO: 5 of the instant application shares 100% sequence identity with amino acids 1 to 207 of SEQ ID NO: 2 of the '145 patent. Applicants contend that because the amino acid sequence of SEQ ID NO: 5 of claim 1(a) of the instant application and amino acids 1 to 207 of SEQ ID NO: 2 of claim 1(a) of the '145 patent share 100% identity, the subject matter of either claim would, if prior art, have anticipated the subject matter of the other claim.

The sequence alignment provided in Exhibit B indicates that the amino acid sequence of SEQ ID NO: 6 of the instant application shares 100% sequence identity with amino acids 30 to 207 of SEQ ID NO: 2 of the '145 patent. The amino acid sequence of SEQ ID NO: 6 is, therefore, a fragment of amino acid residues 1 to 207 of SEQ ID NO: 2 of the '145 patent. Applicants contend that because the amino acid sequence of SEQ ID NO: 6 is the mature form of the amino acid sequence of SEQ ID NO: 2 of the '145 patent (as well as of the amino acid sequence of SEQ ID NO: 5 of the instant application), the amino acid sequence of SEQ ID NO: 6 would have anti-viral

activity, inhibit bone marrow proliferation, activate the Jak/Stat pathway, or bind an antibody that specifically binds a protein having the amino acid sequence of SEQ ID NO: 2. Applicants also contend that because the amino acid sequence of SEQ ID NO: 6 of claim 2 of the instant application shares 100% identity with a fragment of the amino sequence of SEQ ID NO: 2 of the '145 patent, and the mature form would have anti-viral activity, inhibit bone marrow proliferation, activate the Jak/Stat pathway, or bind an antibody that specifically binds a protein having the amino acid sequence of SEQ ID NO: 2, the subject matter of either claim 51 of the '145 patent and claim 2 of the instant application would, if prior art, have anticipated the subject matter of the other claim.

Applicants contend that the Declaration Pursuant to 37 C.F.R. § 1.131 which is provided in Exhibit C, and which was submitted on June 24, 2004 for U.S. Application No. 09/927,850 (from which the instant application claims the benefit of priority as a continuation application), establishes that Applicants will prevail on priority were an interference between the instant application and the '145 patent to be declared. In particular, the Declaration provides copies of forty-one (41) pages from the inventors' laboratory notebook showing conception of the claimed invention before July 21, 1998. The laboratory notebook pages show that a genomic cloning approach was used to identify the nucleic acid sequence of human interferon-like polypeptide (*see* page 34 of laboratory notebook pages). Specifically, three genomic clones were identified as containing nucleic acid sequences encoding at least a portion of human interferon-like polypeptide (clones 2, 6, and 7; *see* page 40 of laboratory notebook pages). The nucleic acid sequences from these clones were isolated and then re-cloned into a suitable sequencing vector. One of the three genomic clones was determined to contain a partial nucleic acid sequence for human interferon-like polypeptide and another genomic clone (clone 6) was determined to contain a full-length nucleic acid sequence for human interferon-like polypeptide (*see* page 62 of laboratory notebook pages). The amino acid sequence of human interferon-like polypeptide was determined from the latter nucleic acid sequence.

The Declaration also provides copies of ten (10) pages from a Research Summary prepared by the inventors showing that the invention disclosed and claimed in the instant patent application was diligently reduced to practice. Specifically, the Research Summary shows that the inventors performed experiments in order to determine the function of protein encoded by the nucleic acid sequence described above, and that once the function of the protein had been determined, the inventors prepared a Research Summary and submitted that Summary to the legal department of

Amgen Inc., the assignee of the instant application. More particularly, the Research Summary shows that several versions of the human and rat IFN-L proteins were produced in a mammalian expression system (*see* page 7 of Research Summary) and that rat IFN-L:Fc fusion protein treatment of several cell lines was found to cause phosphorylation of cellular proteins (*see* page 10 of Research Summary). Thus, the Declaration and attachments provided in Exhibit C establish that Applicants will prevail on priority were an interference between the instant application and the '145 patent to be declared.

Applicants note that claims 1(a) and 2 of the instant application were not added or amended in order to provoke an interference. Applicants contend, therefore, that pursuant to 37 C.F.R. § 41.202(a)(5), a claim chart showing the written description for claims 1(a) and 2 in the specification need not be provided.

Finally, Applicants submit the following chart showing where the instant disclosure provides a constructive to reduction of practice within the scope of the interfering subject matter:

<b>Count 1</b>	<b>Reduction to Practice in Instant Disclosure</b>
An isolated polypeptide comprising the amino acid sequence of amino acids 1 to 207 of SEQ ID NO:2. of U.S. Patent No. 6,433,145.	page 4, lines 9-12; page 7, lines 28-30; page 11, lines 4-5; page 95, lines 10-16; and Figures 2A-2B.
<b>Count 2</b>	<b>Reduction to Practice in Instant Disclosure</b>
An isolated polypeptide comprising the amino acid sequence of a fragment of amino acid residues 1 to 207 of SEQ ID NO:2, wherein the fragment has anti-viral activity.	page 4, lines 16-19; page 12, line 28 to page 13, line 3; page 7, lines 28-30; page 95, lines 10-16; page 103, lines 20-27; and Figures 2A-2B.

In view of the above discussion, Applicants respectfully suggest that an interference be declared between the instant application and the '145 patent.

### **CONCLUSIONS**

Applicants respectfully contend that all conditions of patentability are met in the pending claims as amended. Allowance of the claims is thereby respectfully solicited.

If Examiner Seharaseyon believes it to be helpful, he is invited to contact the undersigned representative by telephone at 312-913-0001.

Respectfully submitted,  
**McDonnell Boehnen Hulbert & Berghoff LLP**

Dated: December 23, 2008

By: /Donald L. Zuhn, Jr./  
Donald L. Zuhn, Jr., Ph.D.  
Reg. No. 48,710



## Exhibit A

	10	20	30	40	50	60
SEQID2	MSTKPD	MIQKCLWLEILMGIFIAGT	LSLDCNLLNVHLRRVTWQ	NLRHLSSMSNSFPVECL		
SEQID5	MSTKPD	MIQKCLWLEILMGIFIAGT	LSLDCNLLNVHLRRVTWQ	NLRHLSSMSNSFPVECL		
	*****					
Prim.cons.	MSTKPD	MIQKCLWLEILMGIFIAGT	LSLDCNLLNVHLRRVTWQ	NLRHLSSMSNSFPVECL		

	70	80	90	100	110	120
SEQID2	RENIAFELPQEFLQYTQPMKRDIK	KAFYEMSLQAFNIFSQHTFKYWKERHLKQIQIGLDQ				
SEQID5	RENIAFELPQEFLQYTQPMKRDIK	KAFYEMSLQAFNIFSQHTFKYWKERHLKQIQIGLDQ				
	*****					
Prim.cons.	RENIAFELPQEFLQYTQPMKRDIK	KAFYEMSLQAFNIFSQHTFKYWKERHLKQIQIGLDQ				

	130	140	150	160	170	180
SEQID2	QAEYLNQCLEEDENENEDMKEMKENEMKPSEARVPQLSSLELRRYFHRIDNFLKEKKYSD					
SEQID5	QAEYLNQCLEEDENENEDMKEMKENEMKPSEARVPQLSSLELRRYFHRIDNFLKEKKYSD					
	*****					
Prim.cons.	QAEYLNQCLEEDENENEDMKEMKENEMKPSEARVPQLSSLELRRYFHRIDNFLKEKKYSD					

	190	200
SEQID2	CAWEIVRVEIRRCLYYFYKFTALFRRK	
SEQID5	CAWEIVRVEIRRCLYYFYKFTALFRRK	
	*****	
Prim.cons.	CAWEIVRVEIRRCLYYFYKFTALFRRK	

## **Exhibit B**

	10	20	30	40	50	60
SEQID2	MSTKPD	MIQKCL	WLEILM	GIFIAG	TLSLDC	NLLNVHLRRVTWQNLRLHLSMSNSFPVECL
SEQID6	-----	-----	-----	-----	-----	-----CNLLNVHLRRVTWQNLRLHLSMSNSFPVECL
						*****
Prim.cons.	MSTKPD	MIQKCL	WLEILM	GIFIAG	TLSLDC	NLLNVHLRRVTWQNLRLHLSMSNSFPVECL

	70	80	90	100	110	120
SEQID2	RENIAF	ELPQEF	LQYTQP	MKRDIK	KAFYEM	SLQAFNIFSQHTFKYWKERHLKQIQIGLDQ
SEQID6	RENIAF	ELPQEF	LQYTQP	MKRDIK	KAFYEM	SLQAFNIFSQHTFKYWKERHLKQIQIGLDQ
						*****
Prim.cons.	RENIAF	ELPQEF	LQYTQP	MKRDIK	KAFYEM	SLQAFNIFSQHTFKYWKERHLKQIQIGLDQ

	130	140	150	160	170	180
SEQID2	QAEYLN	QCLEED	ENENED	MKEMKEN	EMKPSE	ARVPQLSSLELRRYFHRIDNFLKEKKYSD
SEQID6	QAEYLN	QCLEED	ENENED	MKEMKEN	EMKPSE	ARVPQLSSLELRRYFHRIDNFLKEKKYSD
						*****
Prim.cons.	QAEYLN	QCLEED	ENENED	MKEMKEN	EMKPSE	ARVPQLSSLELRRYFHRIDNFLKEKKYSD

	190	200
SEQID2	CAWEIV	RVEIRRCLYYFYKFTALFRRK
SEQID6	CAWEIV	RVEIRRCLYYFYKFTALFRRK
		*****
Prim.cons.	CAWEIV	RVEIRRCLYYFYKFTALFRRK

**Exhibit C**



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE  
(Case No. 99-372-F)

PATENT

In re Application of: Welcher al. )

Serial No.: 09/927,850 )

Before the Examiner: J. Andres

Filed: August 10, 2001 )

Group Art Unit: 1646

For: Interferon-Like Molecule  
and Uses Thereof )

Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Sir:

**DECLARATION ON PURSUANT TO 37 C.F.R § 1.131**

We, Andrew A. Welcher, residing at 1175 Church Street, Ventura, California; Duanzhi Wen, residing at 3885 Campus Drive, Thousand Oaks, California; and Michael Kelley, residing at 3866 Alta Mesa Drive, Studio City, California; hereby declare:

1. We are named co-inventors on United States Application No. 09/927,850, filed on August 10, 2001.
2. The invention disclosed and claimed in the instant patent application was conceived in the United States by us before July 21, 1998 and was then diligently reduced to practice.
3. Accompanying this Declaration are photocopies of forty-one (41) pages from our laboratory notebook showing conception of our invention before July 21, 1998. Specifically, the photocopies of our laboratory notebook show that a genomic cloning approach was used to identify the nucleic acid sequence of human interferon-like polypeptide (*see* page 34 of laboratory notebook). Three genomic clones were identified as containing nucleic acid sequences encoding at least a portion of human interferon-like polypeptide (*i.e.*, clones 2, 6, and 7; *see* page 40). The nucleic acid sequences from these clones were isolated and then re-cloned into a suitable sequencing vector. One of the three genomic clones was determined to contain a partial nucleic acid sequence for human interferon-like polypeptide and another genomic clone (*i.e.*, clone 6) was determined to contain a full-length nucleic acid sequence for human interferon-like polypeptide (*see* page 62). The amino

acid sequence of human interferon like polypeptide was determined from the latter nucleic acid sequence.

4. The dates on the laboratory notebook pages have been redacted from the photocopies. However, the dates are before July 21, 1998, the date on which U.S. Provisional Application No. 60/093,643 was filed, from which U.S. Application No. 09/487,792 claims the benefit of priority, from which U. Patent No. 6,433,145 issued on August 13, 2002.

5. Also accompanying this Declaration are photocopies of ten (10) pages from a Research Summary showing that the invention disclosed and claimed in the instant patent application was diligently reduced to practice. Specifically, the photocopies of the Research Summary show that experiments were performed in order to determine the function of protein encoded by the nucleic acid sequence described in paragraph 3 above, and that once the function of the protein had been determined, Research Summary was prepared and submitted to the legal department of Amgen Inc., the assignee of the instant application. More particularly, photocopies of the Research Summary show that several versions of the human and rat IFN-L proteins were produced in a mammalian expression system (*see* page 7) and that rat IFN-L:Fc fusion protein treatment of several cell lines was found to cause phosphorylation of cellular proteins (*see* page 10).

6. The dates on the Research Summary pages have been redacted from the photocopies.

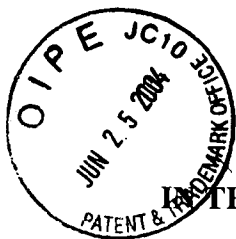
7. We hereby declare further that all statements made herein by each of us to our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Dated: June 10, 2004

Signed: Andrew A. Welcher  
Andrew A. Welcher

Duanzhi Wen  
Duanzhi Wen

Michael Kelly  
Michael Kelly



THE UNITED STATES PATENT AND TRADEMARK OFFICE  
(Case No. 99-372-F)

PATENT

In re Application of: Welcher et al. )

Serial No.: 09/927,850 )

Before the Examiner: J. Andres

Filed: August 10, 2001 )

Group Art Unit: 1646

For: Interferon-Like Molecules )  
and Uses Thereof )

Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Sir:

**DECLARATION PURSUANT TO 37 C.F.R § 1.131**

We, Andrew A. Welcher, residing at 1175 Church Street, Ventura, California; Duanzhi Wen, residing at 3885 Campus Drive, Thousand Oaks, California; and Michael Kelley, residing at 3866 Alta Mesa Drive, Studio City, California; hereby declare:

1. We are named co-inventors on United States Application No. 09/927,850, filed on August 10, 2001.

2. The invention disclosed and claimed in the instant patent application was conceived in the United States by us before July 21, 1998 and was then diligently reduced to practice.

3. Accompanying this Declaration are photocopies of forty-one (41) pages from our laboratory notebook showing conception of our invention before July 21, 1998. Specifically, the photocopies of our laboratory notebook show that a genomic cloning approach was used to identify the nucleic acid sequence of human interferon-like polypeptide (*see* page 34 of laboratory notebook). Three genomic clones were identified as containing nucleic acid sequences encoding at least a portion of human interferon-like polypeptide (*i.e.*, clones 2, 6, and 7; *see* page 40). The nucleic acid sequences from these clones were isolated and then re-cloned into a suitable sequencing vector. One of the three genomic clones was determined to contain a partial nucleic acid sequence for human interferon-like polypeptide and another genomic clone (*i.e.*, clone 6) was determined to contain a full-length nucleic acid sequence for human interferon-like polypeptide (*see* page 62). The amino

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Dated: June 25, 2004

Signed: \_\_\_\_\_  
Andrew A. Welcher

\_\_\_\_\_  
Duanzhi Wen



---

Michael Kelly

Project No. \_\_\_\_\_

Book No. \_\_\_\_\_

TITLE \_\_\_\_\_

IFN

34

ge No. \_\_\_\_\_

hrpe3-00078-F6.

① related to rIFN  $\beta$  (30%).② ① In Certain lot of pancreas mRNA (human) Northern.  
(J. Cao).

③ Screening of pancreas cDNA (human) Library ②.

? Different lot of RNA source

? Different level of expression

Decision: ① re-Screening human pancreas Library  
② determine the genomic screening  
condition

③ Is genomic screening feasible?

IFN probe  
for genomic blot

PAGE: 1

13:16

17

ID: CHERENCOV

0.5

USER: 2

COMMENT:

PRESET TIME :

0.50

DATA CALC :

CPM

H# : NO

SAMPLE REPEATS:

1

PRINTER

: STD

COUNT BLANK :

NO

IC# : YES

REPLICATES :

1

RS232

: OFF

TWO PHASE :

NO

AQC : NO

CYCLE REPEATS :

1

SCINTILLATOR:

XTAL

LUMEX: NO

LOW SAMPLE REJ:

0

LOW LEVEL :

NO

HALF LIFE CORRECTION DATE:

none

ISOTOPE 1:

32P

%ERROR: 0.00

FACTOR:

1.000000

BKG. SUB:

0

SAM PGS  
NOTIME - IG#  
MIN33P  
CPM %ERRORLUMEX  
%ELAPSED  
TIME

1 \*\* -1

0.50 655.1

427775.8

0.43

0.00

0.83

4.3x10<sup>5</sup> cpm/λ

To Page No. \_\_\_\_\_

Page No. \_\_\_\_\_

PCR - Hot rIFN probe:

template	1 $\lambda$
1795-01	20 pm
1795-02	1 $\lambda$
10X PCR Buf.	10 $\lambda$
100 mM dNTPs	10 $\lambda$
$^{32}$ P-dCTP	5 $\lambda$
25 mM MgCl <sub>2</sub>	16 $\lambda$
Tag	1 $\lambda$
H <sub>2</sub> O to	100 $\lambda$

94°C 30sec, 50°C 30sec 74°C 1min for 40 cycles.

G-50 column purified.

count:  $4.3 \times 10^5$  cpm/ $\lambda$ .

Determine the hybridization and washing condition for genomic screening.

- ① very likely the homology of hIFN vs. rIFN is in the neighborhood of G<sub>0</sub>.
- ② The formamide should be between 25% - 30%

washing condition should start with gentle wash, then elevate the T wash. Determine a condition in which fragment is detectable while background is minor.

To Page No. \_\_\_\_\_

From the genomic southern (D. Wen keeps all the photo) it is clear:

① There is an 1.8kb *HindIII* fragment that strongly hybridize w/ Probe.

② The formamide concentration can be adjusted to ~30% for relatively optimal signal vs. noise ratio.

③ Washing can be conducted @ ~55°C in 0.2 or 0.3X SSC, 0.1% SDS.

Wen further found in literature:

① IFN $\gamma$  family member is single gene, i.e. no intron.

② A lot of pseudo IFN gene as well.

But what about we identify a gene resemble *mppe3-0078-F6*, also proved its expressing tissues?

Page No. \_\_\_\_\_

Screening h. Pancreas Library w/ Rat Probe

RTN - probe for human pancreas Library screening

PAGE: 1

ID: CHERENCOV 0.5

USER: 2

COMMENT: .

PRESET TIME : 0.50

DATA CALC : CPM

COUNT BLANK : NO

TWO PHASE : NO

SCINTILLATOR: XTAL

LOW LEVEL : NO

H# : NO SAMPLE REPEATS: 1

IC# : YES REPLICATES : 1

AQC : NO CYCLE REPEATS : 1

LUMEX: NO LOW SAMPLE REJ: 0

HALF LIFE CORRECTION DATE: none

PRINTER

: STD

RS232

: OFF

ISOTOPE 1:

32P

%ERROR: 0.00

FACTOR: 1.000000

BKG. SUB:

0

SAM NO	POS	TIME MIN	IC#	32P CPM	%ERROR	LUMEX %	ELAPSED TIME
1	**	-1	0.50	606.2	827666.2	0.31	0.01 0.91

PCR as on p. 35.

Library screening

- 1x 10<sup>6</sup> clones on 20 plates

- 30% formaldehyde. 5x SSC. 42°C O/N

- Wash: 2x SSC, 0.1% SDS 30min @ 50°C

- O/N exposure

And

There is no double positive clones.

To Page No. \_\_\_\_\_

Issued &amp; Understood by me,

Date

Invented by

Date

Project No. \_\_\_\_\_

Book No. \_\_\_\_\_

TITLE \_\_\_\_\_

IFN

38

e No. \_\_\_\_\_

Screening human fibroblast genomic Library.

Library: human lung fibroblast genomic Library in  
Fix II vector (Stratagene).1x10<sup>6</sup> independent clones on nitro-  
cellulose membrane.

PCR probe: as described on p.35

198  
IFN probe for genomic Screening

PAGE: 1

12:47

D: CHERENCOV 0.5

IER: 2 COMMENT:

RESET TIME :	0.50								
ITA CALC :	CPM	H# :	NO	SAMPLE REPEATS:	1	PRINTER	:	STD	
UNT BLANK :	NO	IC# :	YES	REPLICATES :	1	RS232	:	OFF	
IO PHASE :	NO	AQC :	NO	CYCLE REPEATS :	1				
INTILLATOR:	XTAL	LUMEX:	NO	LOW SAMPLE REJ:	0				
OW LEVEL :	NO	HALF LIFE CORRECTION DATE:				none			

ISOTOPE 1: 32P %ERROR: 0.00 FACTOR: 1.000000 BKG. SUB: 0

AM	POS	TIME	IC#	32P	LUMEX	ELAPSED
JO		MIN		CPM %ERROR	%	TIME
1	** -1	0.50	632.0	704931.5	0.34	0.01 0.89

To Page No. \_\_\_\_\_

Page No. \_\_\_\_\_

Life Library to Nitrocellulose membrane.

① 5 min denature, 5 min neutralization. 15 Sec 2X SSC

② 80°C bake 1 hr.

③ pre-hyb: 30% Formamide  
5X SSC  
2X Denhart's  
100 µg/ml ssDNA  
0.2% SDS  
2 mM EDTA  
0.1% Pyrophosphate

42°C O/N

④ Wash.

At R.T. 1X SSC, 0.1% SDS. 2x 30 min

At 55°C 0.2X SSC, 0.1% SDS 15 min

~80°C BioMax Kodak film O/N at -80°C

Project No. \_\_\_\_\_

Book No. \_\_\_\_\_

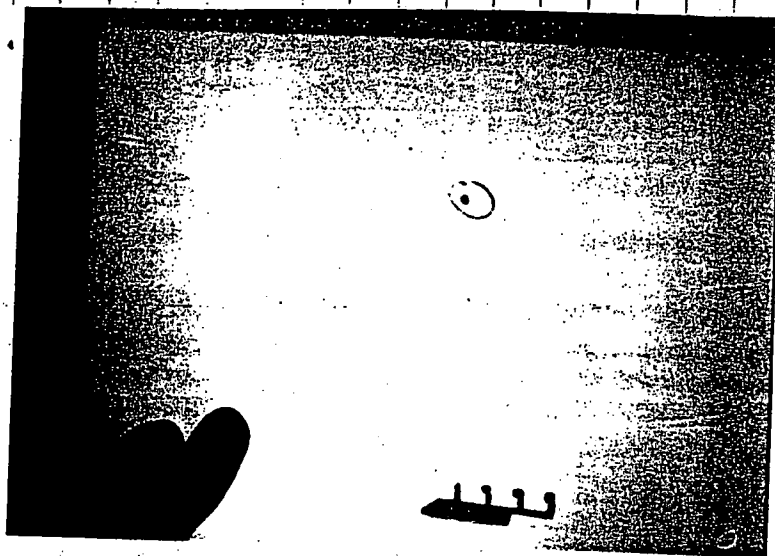
TITLE \_\_\_\_\_

IFN

40

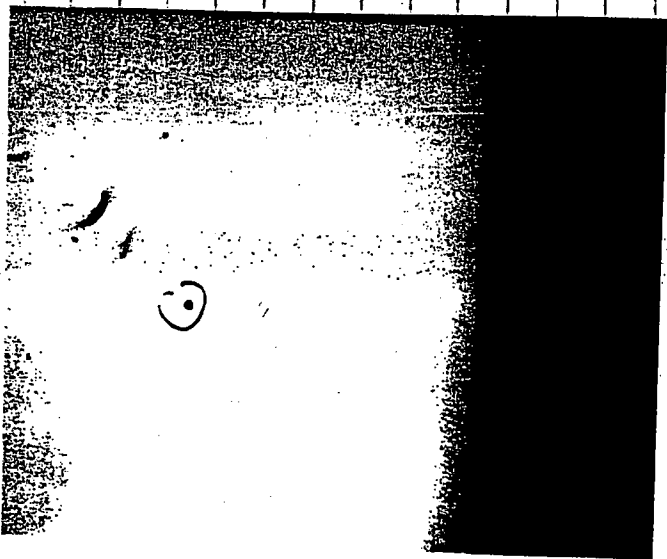
ie No. \_\_\_\_\_

Primary screening Result.



# 2

# 6



1) pick up the  $\phi$  colony with  
SM elution 37°C 2 hrs.

2)  $1/500$  dilution for secondary

3) double-lift secondary  
screening membrane.

# 7. All double positive

To Page No. \_\_\_\_\_



Page No. \_\_\_\_\_

2nd screening - 6 IZN

4/19/98  
IZN probe

PAGE: 1

ID: CHERENCOV 0.5

USER: 2

COMMENT:

20:13

PRESET TIME : 0.50

DATA CALC : CPM

COUNT BLANK : NO

TWO PHASE : NO

SCINTILLATOR: XTAL

LOW LEVEL : NO

H# : NO SAMPLE REPEATS: 1

IC# : YES REPLICATES : 1

AQC : NO CYCLE REPEATS : 1

LUMEX: NO LOW SAMPLE REJ: 0

HALF LIFE CORRECTION DATE:

PRINTER : STD

RS232 : OFF

none

ISOTOPE 1: 32P %ERROR: 0.00 FACTOR: 1.000000 BKG. SUB: 0

SAM NO	POS	TIME MIN	IC#	32P CPM	%ERROR	LUMEX %	ELAPSED TIME
1	** -1	0.50	615.7	458314.7	0.42	0.01	0.86

Hybridization: 30% formaldehyde  
5XSSC  
42°C o/n.

Wash: 1XSSC, 0.1% SDS R.T. 30min

0.2XSSC, 0.1% SDS 55°C 15min

To Page No. \_\_\_\_\_

essed &amp; Understood by me,

Date

Invented by

Date

Project No. \_\_\_\_\_

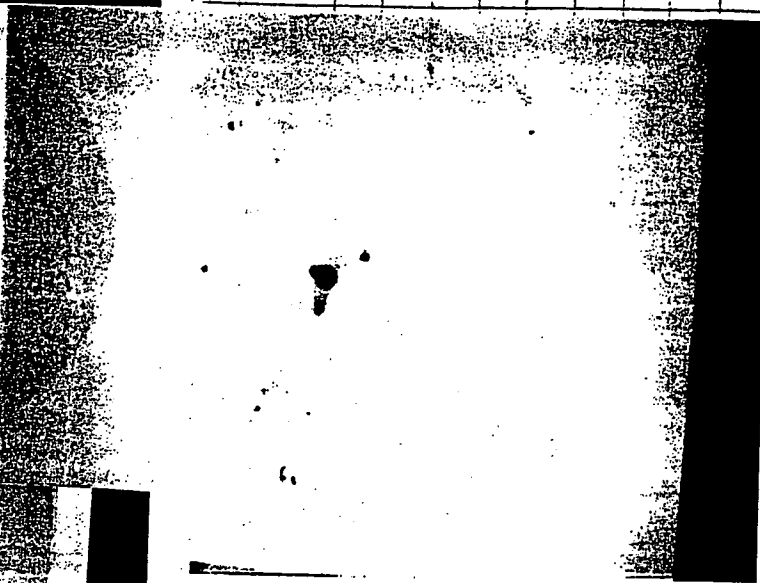
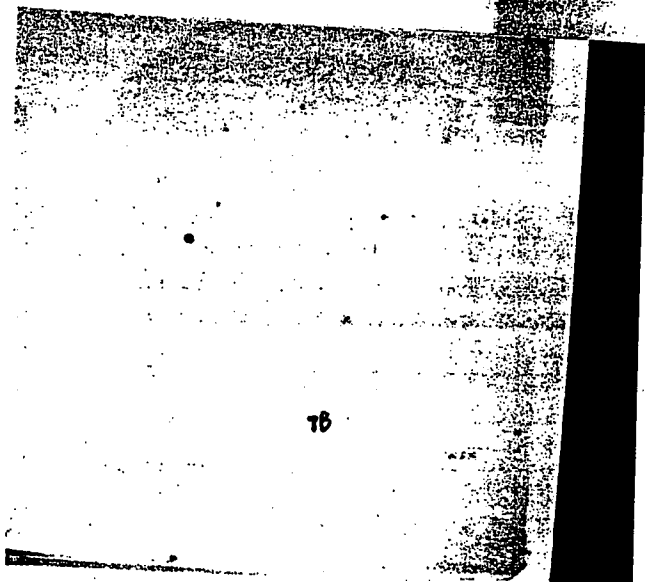
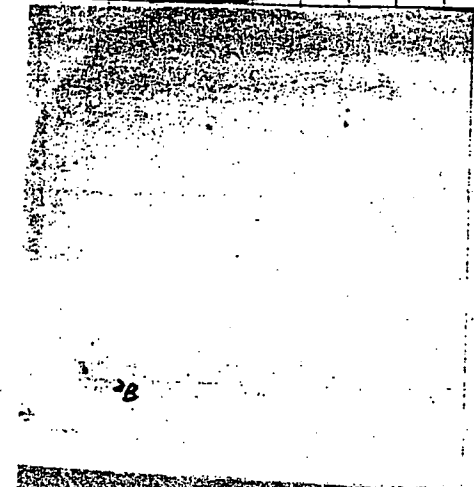
Book No. \_\_\_\_\_

TITLE \_\_\_\_\_

IN

42

ge No. \_\_\_\_\_



pick-up 2nd clone . elute with SM.

prepare for phage DNA preparation.

n Page No. \_\_\_\_\_

# ~~XXXXXXXXXX~~ $\phi$ DNA preparation protocol,

Preparation of lamdan phage DNA  
Grow up the phage (on plates or in liquid medium).  
Collect the supernatant and spin down with 3000 rpm.  
Add DNase I (10u/ml) and RNase (20mg/ml) incubate 30 min at 4 degree.  
Add 1/3 volume 30% PEG 6000 in 3M NaCl put in ice for 1 hr or at 4 degree overnight.  
12000g centrifugation 20 min  
Discard supernatant and invert the tube on papers to remove S completely.  
Add 1/10-1/5 of origin volume T10E1 to suspend the phage particles.  
Add 0.5M EDTA to a final concentration of 20mM and proteinase K 10mg/ml, incubate 1hr in 55 degree waterbath.  
Add 5% CATS in 0.5M NaCl to a final concentration of 0.1% and put at 65 degree for 5 min.  
Spin down and dissolve in 1.2M NaCl.  
Add 2.5 vol. of ethanol and spin down.  
Discard the ethanol and wash once with 70% ethanol.  
Dry the pellets and dissolve in T10E1 in ice 30 min. then at 4 degree for 10 min. don't put on RT. stock in 4 degree.

- phage has to be amplified once before proceeding to  $\phi$  DNA prep. on a 100mm plate. 10ul  $\phi$  + top agar  $\rightarrow$  o/n 37°C.

SM elute

- on LB/Agarose plate, grow  $\phi$  o/n @ 37°C

- elute w/ SM 2 1/2 hrs @ 3-7.

To Page No. \_\_\_\_\_

Project No. \_\_\_\_\_

Book No. \_\_\_\_\_

TITLE \_\_\_\_\_

IFN

44

e No. \_\_\_\_\_

BECKMAN DU-600

Human Genomic IFN like clone  
Φ prep:Date: \_\_\_\_\_  
Time: 23:19leic Acid  
adSamples

Method

SaveClear

Print

Quit

Results file: A:\WORK\_RES

Method name: A:\DEFAULT

Assay type: General Ratio and Concentration

Formula setup: VIEW

Sampling device: None

Read average time: 0.50 sec

Units: UG/UL

Background Correction: [No ]

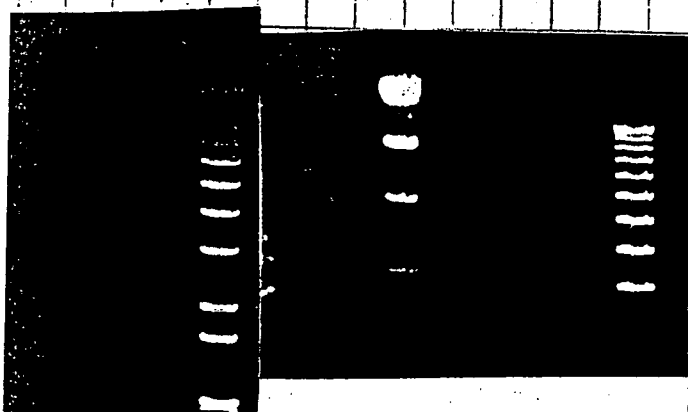
Concentration: [Yes]

Peak Pick: [No ]

↓ ↑

Sample	abs 260.0 nm	abs 280.0 nm
#2	0.1428	0.0774
#6	0.3206	0.1775
#7	0.1731	0.0913

260.0 nm 280.0 nm	280.0 nm 260.0 nm	x100 SSRNA UG/UL	X100 dsDNA UG/UL
1.8453	0.5419	0.5711	0.7139
1.8066	0.5535	1.2823	1.6029
1.8962	0.5274	0.6922	0.8653



#2: 143 ng/λ

#6: 32.1 ng/λ

#7: 17.3 ng/λ

Set-up NotI digestion to  
release insert in pIX.

20 ng Φ DNA

1.2x H

NotI (HC) 40u x 2.5 = 100

H<sub>2</sub>O

ON @ 37°C incubator.

To Page No. \_\_\_\_\_

Page No. \_\_\_\_\_

IFN

~~where~~ where is the IFN fragment?

The two ← indicated on p. 44 insert of interest?

Repeat Not I digestion; run a small agarose 0.5% gel.

Transfer and Southern to determine the band

Hyb. 30% Formamide, wash: 0.2xSSC, 0.1% SDS.  
55°C 15min

Results on p. 46

BECKMAN DU-600

Date: \_\_\_\_\_  
Time: 16:18

Nucleic Acid  
ReadSamples

Method

SaveClear

Print

Quit

Results file: A:\WORK\_RES

Method name: A:\DEFAULT

Assay type: General Ratio and Concentration

Units: UG/UL

Formula setup: VIEW

Background Correction: [No]

Sampling device: None

Concentration: [Yes]

Read average time: 0.50 sec

Peak Pick: [No]

Sample ID	abs		260.0 nm		x100 ssRNA UG/UL	X100 dsDNA UG/UL
	260.0 nm	280.0 nm	280.0 nm	260.0 nm		
1 #2	0.0059	0.0027	2.1876	0.4571	0.0235	0.0293
2 #6	0.0082	0.0043	1.8895	0.5292	0.0326	0.0408
3 #7	0.0085	0.0046	1.8522	0.5399	0.0338	0.0423
4						

1/20  
#2 5.9 x 50 x 20 = 6 ng/λ  
#6 8.2 x 1000 = 8 ng/λ  
#7 8.5 x 1000 = 8.5 ng/λ

Ligation: 10 ng cut vect.  
+ 6 λ Insert  
+ 2 λ 10x Buff  
50 μl 4/15/90

Assessed &amp; Understood by me,

Date

Invented by

Date

Project No. \_\_\_\_\_

Book No. \_\_\_\_\_

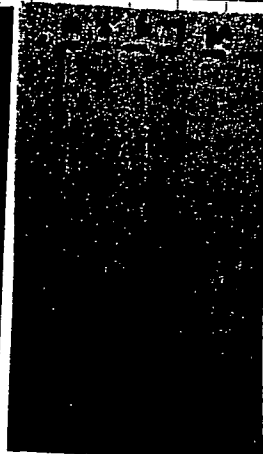
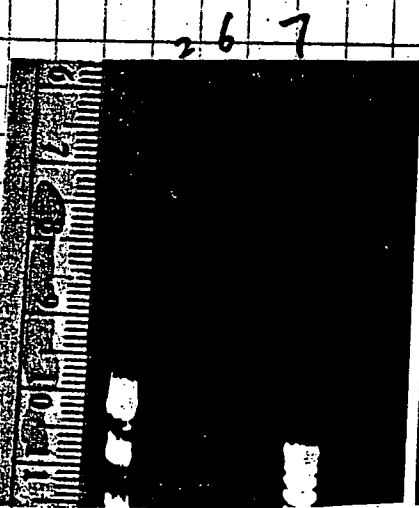
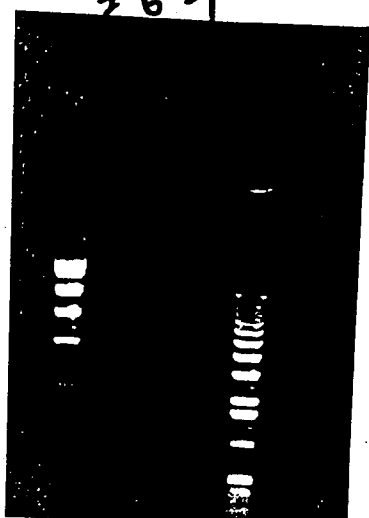
TITLE \_\_\_\_\_

ITN

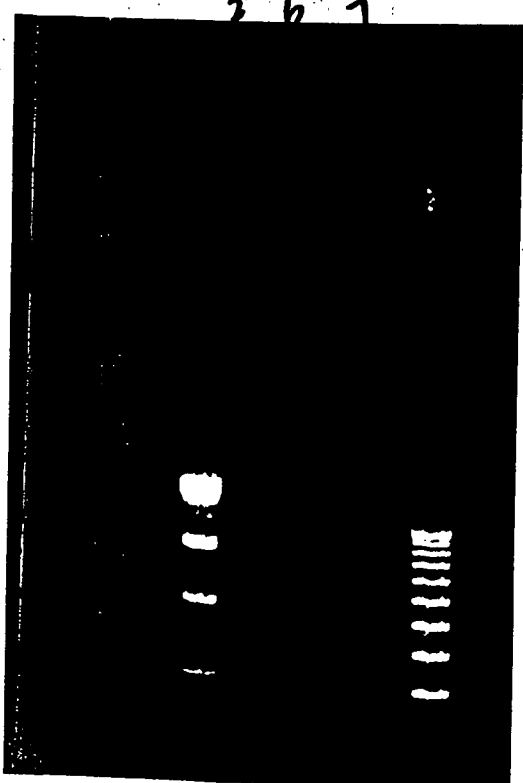
46

Page No. \_\_\_\_\_

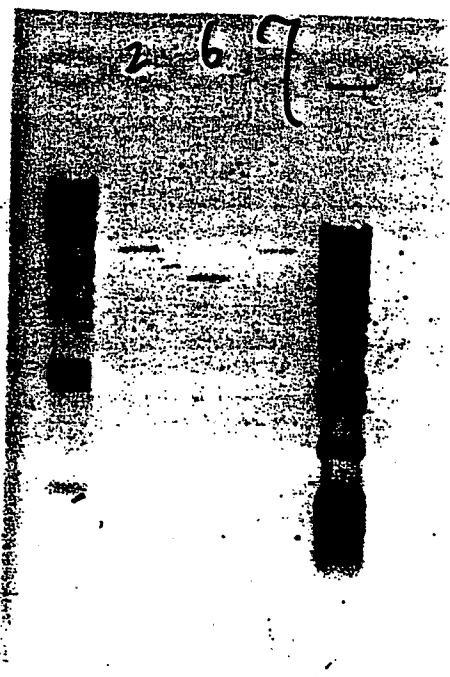
[REDACTED]



[REDACTED] Gel purifying ~~ITN~~ genomic fragment



STRATAGENE EAGLE EYE II  
IMAGE SIZE (640 x 480 x 8).  
INT PERIOD = 0.36 SEC.  
ACQUIRED [REDACTED] 13:52:19



STRATAGENE EAGLE EYE II  
IMAGE SIZE (640 x 480 x 8).  
INT PERIOD = 0.39 SEC.  
ACQUIRED [REDACTED] 16:04:28

Read & Understood by me.

Date

Invented by

W. Chen

Date

Page No. \_\_\_\_\_

pSV. Sport/NotI genomic fragment

BECKMAN DU-600

Nucleic Acid  
Read Samples

Method

Results file: A:\WORK\_RES

Assay type: General Ratio and Concentration

Formula setup: VIEW

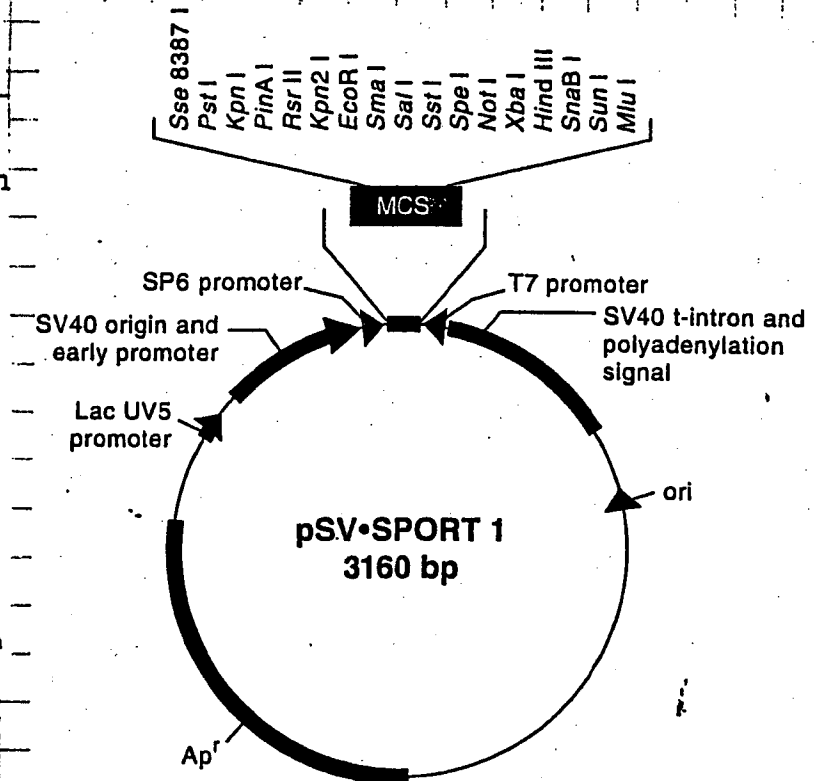
Sampling device: None

Read average time: 0.50 sec

Sample ID	abs 260.0 nm	abs 280.0 nm
1 pSV.pSport	0.0107	0.0039
2 pSV.pSport	0.0204	0.0093
3 pSV.pSport		

1 pSV.pSport  
2 pSV.pSport  
3 pSV.pSport

pSV.pSport/NotI 20 ng/μl



0.8% TAE - agarose gel / NotI digestion

STRATAGENE EAGLE EYE II 12:46:39

SIZE (640 x 480 x 8).

EXPOSURE = 0.13 SEC.

RED

72 61 71

72 61 71

72 61 71

72 61 71

72 61 71

72 61 71

72 61 71

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72 61 71

72 61 71

72 61 71

72 61 71

72 61 71

72 61 71

72 61 71

72 61 71

72 61 71

72 61 71

72 61 71

miniprep DNA 5μl

10X H 1μl

NotI 0.5μl (10u)

H<sub>2</sub>O 3.5μl

Total 10μl @ 37°C 1 1/2 hrs.

← Insert  
← pSV.pSport

To Page No. \_\_\_\_\_

Project No. \_\_\_\_\_

Book No. \_\_\_\_\_

TITLE \_\_\_\_\_

1.1. 17N

48

ge No. \_\_\_\_\_

## Set-up genomic clone Analysis.

5 $\lambda$  mini-prep DNA  
 1 $\lambda$  10x Buffer (BMB)  
 0.5 $\lambda$  EZ.  
 3.5 $\lambda$  H<sub>2</sub>O

10 $\lambda$  @ 37°C 1 1/2 hrs.

Restriction EZs:

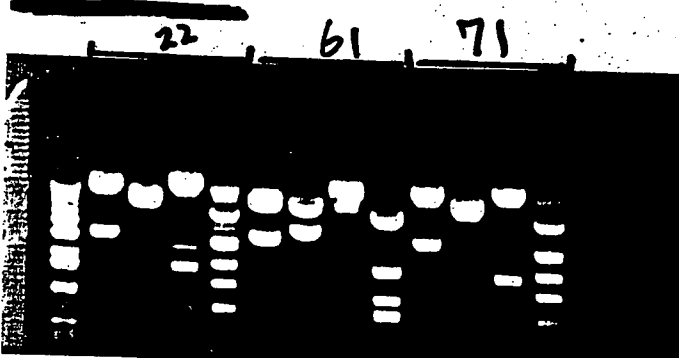
present on MCS of psu.pspart

NotI, EcoRI, XbaI &amp; HindIII

87% TAE gel.

STRATAGENE EAGLE EYE II 19:18:42

540 x 480 x 8).  
 ID = 0.46 SEC.



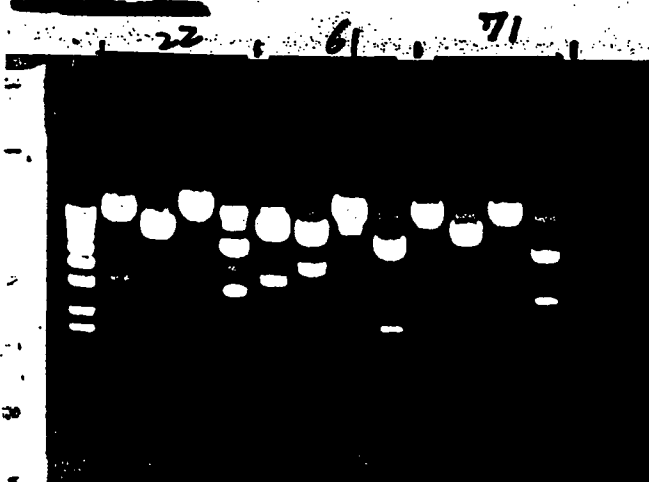
22 and 71 are identical independent clones. but not 61.

	22	61	71
EcoRI	0	2	0
XbaI	3	2	3
HindIII	7/4	7/4	7/4

Is that why initially EcoRI digestion on genomic DNA didn't light up by rmp3 probe?

STRATAGENE EAGLE EYE II 19:35:05

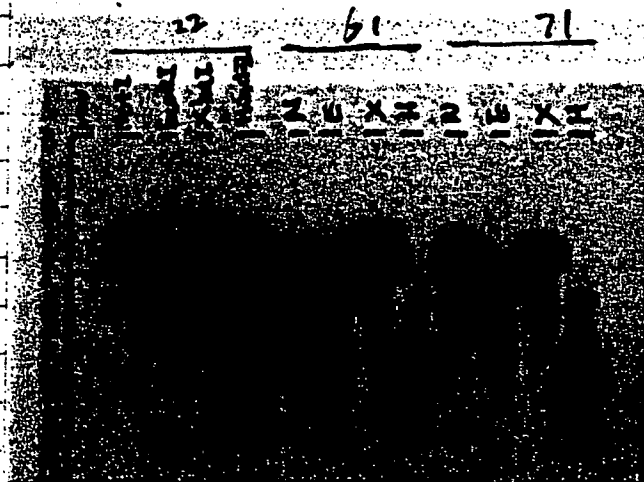
540 x 480 x 8).  
 ID = 0.66 SEC.



22  
61  
71  
EcoRI  
XbaI  
HindIII

NEX H NEX H

Transfer this gel w/ alkaline transfer.



\* HindIII incomplete digestion

To Page No. \_\_\_\_\_



Page No.           

Washing Southern Blot.

Hybridization: 30% Formamide, 5x SSC, 2x Denhart's  
 10<sup>6</sup> SSDNA, 0.2% SDS, 2mM EDTA, 0.1% pyrophos  
 (No NH<sub>2</sub>PO<sub>4</sub>)  
 42°C, 3 hrs. + 5% Dextran Sulfate for Hyb.

PCR - Hot probe: Template 1λ (20ng)  
 1795-01 1λ (20pm)  
 1795-02 1λ (20pm)  
 10mM dNTP 10λ (dCTP @ 0.1mM)  
<sup>32</sup>P-dCTP 5λ  
 10x PCR buf. 10λ  
 25mM MgCl<sub>2</sub> 16λ (4mM final)  
 Taq 1λ  
 H<sub>2</sub>O to 100ul Control: + 60ul H<sub>2</sub>O  
 with 10mM dNTP.

5/7/98 RTN probe

PAGE: 1

22:04

ID: CHERENCOV 0.5

USER: 2

COMMENT:

PRESET TIME :	0.50	H# :	NO	SAMPLE REPEATS:	1	PRINTER	: STD
DATA CALC :	CPM	IC# :	YES	REPLICATES :	1	RS232	: OFF
COUNT BLANK :	NO	AQC :	NO	CYCLE REPEATS :	1		
TWO PHASE :	NO	LUMEX:	NO	LOW SAMPLE REJ:	0		
SCINTILLATOR:	XTAL	HALF LIFE CORRECTION DATE:	none				
LOW LEVEL :	NO						

ISOTOPE 1: 32P %ERROR: 0.00 FACTOR: 1.000000 BKG. SUB: 0

SAM NO	POS	TIME MIN	IC#	32P CPM	%ERROR	LUMEX %	ELAPSED TIME
1	** -1	0.50	592.9	528289.8	0.39	0.01	0.86

1ul count.

Washing: • 1 x SSC, 0.1% SDS @ RT 1hr  
 0.2 x SSC, 0.1% SDS @ 55°C 15min  
 exp. @ -80°C 0/N.

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17N

50

ie No. \_\_\_\_\_

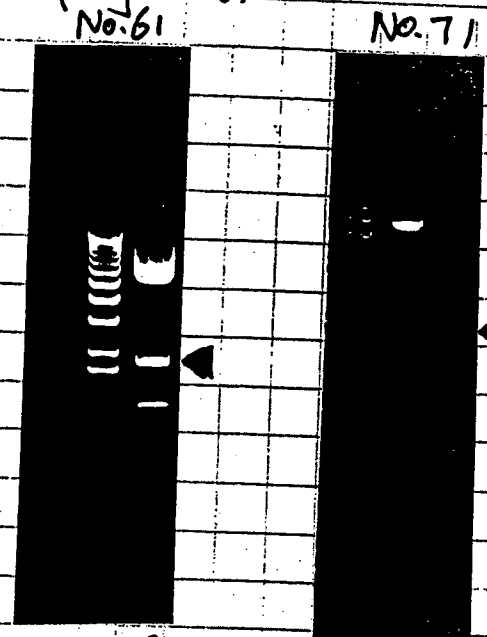
h mrep-3 cloning: Subclone genomic fragment.  
Set-up digestion.

70  $\lambda$  mini-prep DNA  
8  $\lambda$  10x B Buffer (BMB)  
2  $\lambda$  BamHI (20u)  
80  $\lambda$  total @ 37°C 5 hrs

8  $\lambda$  run gel (with dye)  
indicates positive band in  
Southern Blot with mrep-3  
probe (p. 48).

92  $\lambda$  (with dye) run a 0.8% TAE gel.

Qiagen Gel Purification Kit



0.8% TAE-agarose gel

(Hind III fragments)

BECKMAN DU-600

Date: \_\_\_\_\_

Time: 21:25

leic Acid  
adSamples Method SaveClear Print Quit

Results file: A:\WORK\_RES

Method name: A:\DEFAULT

Assay type: General Ratio and Concentration  
Formula setup: VIEW  
Sampling device: None  
Avg average time: 0.50 sec

Units: UG/UL  
Background Correction: [No]  
Concentration: [Yes]  
Peak Pick: [No]

1/10 dilu

Sample	abs	abs	260.0 nm	280.0 nm	x100	X100
	260.0 nm	280.0 nm	260.0 nm	260.0 nm	UG/UL	UG/UL
#61	0.0168	0.0093	1.7933	0.5576	0.0670	0.0838
#71	0.0201	0.0112	1.7963	0.5567	0.0803	0.1003

#61  $0.0168 \times 50 \times 20 \approx 1718/\lambda$

#71  $0.0201 \times 50 \times 20 \approx 2010/\lambda$

No. 61.71

61.71 insert  
is probably  
same (identical)  
size. Hind III  
fragment size)

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&amp; Understood by me.

Date

Invented by

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Ligation:

3  $\lambda$  dephosphorylated psv-pspmt (17ng)  
 1  $\lambda$  10x Lig. Buffer (BMB)  
 1  $\lambda$  T4 DNA Ligase (BMB)  
 5  $\lambda$  Insert (85 ~ 100ng)  
 10  $\lambda$

Control: + 5  $\mu$ l H<sub>2</sub>O in vector control.

14°C 1 hr

Transformation: 140  $\lambda$  DH10 $\alpha$  ElectroMax cell  
 + 1.5  $\lambda$  Ligation Mix

6 transformation clones/each  
for miniprep.

STRATAGENE EAGLE EYE II 13:20:23

E SIZE (640 x 480 x 8).  
 PERIOD = 0.36 SEC.  
 IRED

HindII

61

72

Digest w/ HindII

5  $\lambda$  DNA1  $\lambda$  10x B (BMB)0.5  $\lambda$  HindII (5u)3.5  $\lambda$  H<sub>2</sub>O10  $\lambda$  total 37°C 1/2 hrs

2% TAE gel

All contain insert. (1.8 kb)

Further Analysis w/

KpnI, PstI, SalI (BMB)

5  $\lambda$  DNA1  $\lambda$  10x Buffer0.5  $\lambda$  EZ (5u)3.5  $\lambda$  H<sub>2</sub>O10  $\lambda$  37°C 1/2 hr

So no additional EZ cut in the insert.

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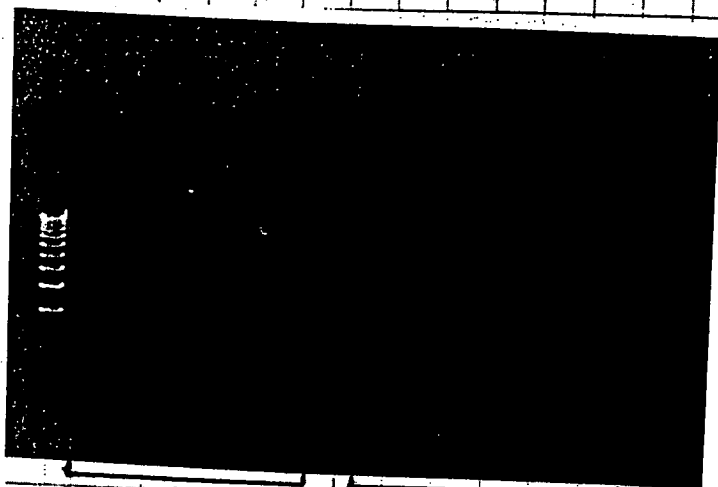
Book No. \_\_\_\_\_

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ZEN

52

age No. \_\_\_\_\_



Transfer to N.C. for future reference

61

71

Sequencing Request

D	Clone	Requestor		Status	Submit	Rcvd
9808902	hgmrep3-6.1	Wen	Chen	Pending	██████	00/00/00
9808903	hgmrep3-6.2	Wen	Chen	Pending	██████	00/00/00
9808904	hgmrep3-6.5	Wen	Chen	Pending	██████	00/00/00
9808905	hgmrep3-7.1	Wen	Chen	Pending	██████	00/00/00
9808906	hgmrep3-7.2	Wen	Chen	Pending	██████	00/00/00
9808907	hgmrep3-7.2 X deleted!	Wen	Chen	Pending	██████	00/00/00
9808908	hgmrep3-7.3	Wen	Chen	Pending	██████	00/00/00

3-6.1 } identical insert in same orientation  
 3-6.5 }  
 3-7.1 }

3-6.2 } identical insert in reverse orientation  
 3-7.2 }

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mCamp2 Southern: Human Genomic DNA

probe: mCamp2 template 2λ (long)  
 1582-15 (5' primer) 2λ (20pm)  
 1536-79 (3' primer) 2λ (20pm)  
 10x Buffer 10λ  
 10mM dNTP (dCTP @ 0.1mM) 10λ  
 α-<sup>32</sup>P dCTP 5λ  
 25mM MgCl<sub>2</sub> 16λ  
 Tag (BMB) 1λ  
 H<sub>2</sub>O 52λ

Cold control + ~~10λ~~ 10mM dNTP + 52 extra H<sub>2</sub>O  
 94°C 30sec → 60°C 30sec  $\frac{1}{min}$  → 45 cycles

PAGE: 1

ID: CHERENCOV 0.5

USER: 2

COMMENT:

16:06

PRESET TIME : 0.50

DATA CALC : CPM

COUNT BLANK : NO

TWO PHASE : NO

SCINTILLATOR: XTAL

LOW LEVEL : NO

H# : NO SAMPLE REPEATS: 1

IC# : YES REPLICATES : 1

AQC : NO CYCLE REPEATS : 1

LUMEX: NO LOW SAMPLE REJ: 0

HALF LIFE CORRECTION DATE:

PRINTER : STD

RS232 : OFF

none

ISOTOPE 1: 32P %ERROR: 0.00 FACTOR: 1.000000 BKG. SUB: 0

SAM NO	POS	TIME MIN	IC#	32P CPM	%ERROR	LUMEX %	ELAPSED TIME
1	** -1	0.50	602.8	1115564	0.27	0.02	0.95

1λ 1.1 x 10<sup>6</sup> cpm/λ

Cold control.

6/ primary Screening:

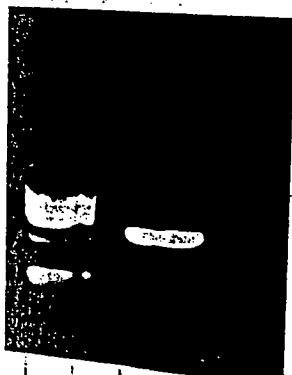


IMAGE SIZE (440 x 480 x 8)  
 INT PERIOD = 0.06 SEC.  
 ACQUIRED

STRATAGENE EAGLE 3

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Chy 22

54

e No. \_\_\_\_\_

Hybridization in 30% Formamide

30% Formamide  
5X SSC

2X Denhardt's

10<sup>6</sup> M<sup>3</sup>/ul ssDNA

0.2% SDS

2mM EDTA

0.1% Pyrophosphate

H<sub>2</sub>O

to 100 ml

Stock  
30ml  
25ml4ml  
1ml

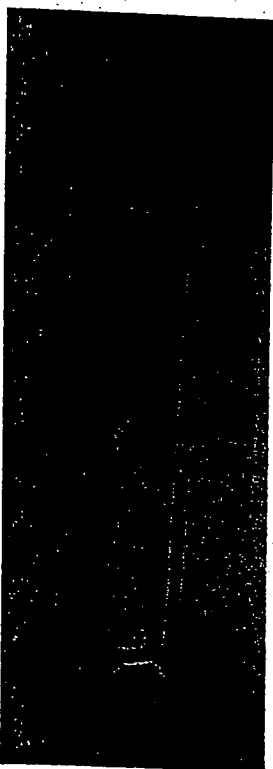
1ml

0.4ml

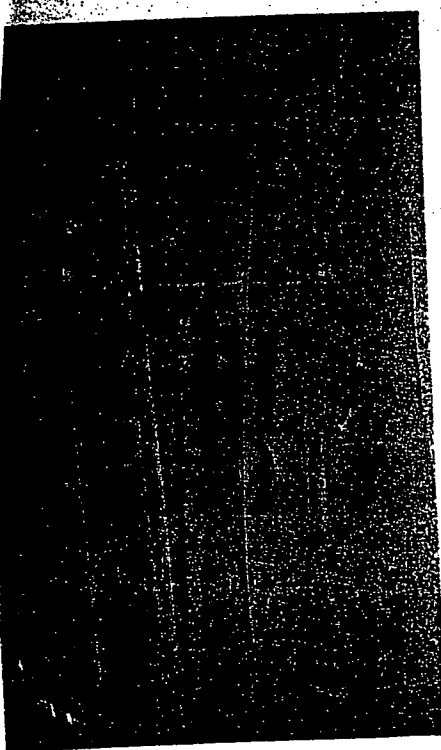
1ml

37.6ml

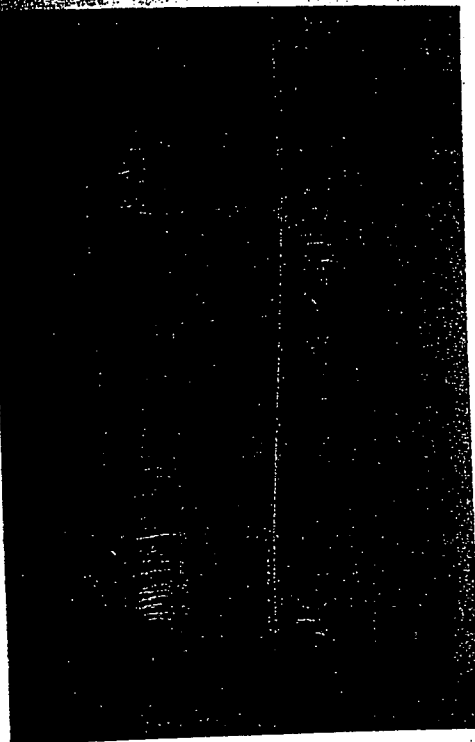
42°C 0/N stripe rehyb.



20X Formamide, 0.2% Denhardt's, 10<sup>6</sup> M<sup>3</sup>/ul ssDNA, 0.2% SDS, 2mM EDTA, 0.1% Pyrophosphate, H<sub>2</sub>O to 100 ml. IMAGE SIZE (640 x 480 x 8). REAL-TIME ACQUIRE.



20X Formamide, 0.2% Denhardt's, 10<sup>6</sup> M<sup>3</sup>/ul ssDNA, 0.2% SDS, 2mM EDTA, 0.1% Pyrophosphate, H<sub>2</sub>O to 100 ml. IMAGE SIZE (640 x 480 x 8). REAL-TIME ACQUIRE.



20X Formamide, 0.2% Denhardt's, 10<sup>6</sup> M<sup>3</sup>/ul ssDNA, 0.2% SDS, 2mM EDTA, 0.1% Pyrophosphate, H<sub>2</sub>O to 100 ml. IMAGE SIZE (640 x 480 x 8). REAL-TIME ACQUIRE.

STRATAGENE EAGLE EYE II 15/07/30

action 30%  
PC (Formamide)  
SSC 0.2X  
SDS 0.1%  
exp 24 hrs

20%  
0.5X  
0.1%  
24 hrs

20%  
0.5X  
0.1%  
24 hrs

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E

IRN

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5

REVERSE-COMPLEMENT of: 9808902.Con check: 3852 from: 1 to: 1163  
When  
DNA-hgmrep3-6.1 p=890-24 end  
assembled by JK: [REDACTED]  
9808902.con

With 1 enzymes: HINDIII

[REDACTED] 17:01 ..

```
CTGAGAAGAGTCACCTGGCAAAATCTGAGACATCTGAGTAGTATGAGCAATTCATTTCCT
1 -----+-----+-----+-----+-----+-----+-----+ 60
GACTCTTCTCAGTGGACCGTTTTAGACTCTGTAGACTCATCATACTCGTTAAGTAAAGGA

a L R R V T W Q N L R H L S S M S N S F P -
GTAGAATGTCTACGAGAAAACATAGCTTTTGAGTTGCCCAAGAGTTTCTGCAATACACC
61 -----+-----+-----+-----+-----+-----+ 120
CATCTTACAGATGCTCTTTTGTATCGAAAACCAACGGGGTTCTCAAAGACGTTATGTGG

a V E C L R E N I A F E L P Q E F L Q Y T -
CAACCTATGAAGAGGGACATCAAGAAGGCTTCTATGAAATGTCCCTACAGGCTTCAAC
121 -----+-----+-----+-----+-----+-----+ 180
GTTGGATACTTCTCCCTGTAGTCTTTCOGGAAGATACTTTACAGGGATGTCCGGAAGTTG

a Q P M K R D I K K A F Y E M S L Q A F N -
ATCTTCAGCCAACACACCTTCAAATATTTGGAAGAGAGACACCTCAAACAATCCAAATA
181 -----+-----+-----+-----+-----+-----+ 240
TAGAAGTCGGTTGTGTGGAAGTTTATAACCTTCTCTCTGTGGAGTTTGTAGGTTTAT

a I F S Q H T F K Y W K E R H L K Q I Q I -
GGACTTGATCAGCAAGCAGAGTACCTGAACCAATGCTTGGAGGAAGACGAGAATGAAAT
241 -----+-----+-----+-----+-----+-----+ 300
CCTGAAGTATGCTTCTCTCATGGACTTGGTTACGAACCTCTCTCTCTTACTTTTAT

a G L D Q Q A E Y L N Q C L E E D E N E N -
GAAGACATGAAAGAAATGAAAGAGAATGAGATGAAACCTCAGAAGCCAGGGTCCCCAG
301 -----+-----+-----+-----+-----+-----+ 360
CTTCTGTACTTTCTTTACTTTCTTACTTCTACTTTGGGAGTCTTCGGTCCCAGGGGGTC

a E D M K E M K E N E M K P S E A R V P Q -
CTGAGCAGCCTGGAAGTGGAGATATTTCCACAGGATAGACAATTTCTGAAAGAAAAG
361 -----+-----+-----+-----+-----+-----+ 420
GACTCGTCCGACCTTGACTCCTCTATAAAGGIGTCTATCTGTTAAAGGACTTCTTTTC

a L S S L E L R R Y F H R I D N F L K E K -
AAATACAGTACTGTGCTGGGAGATTGTCCGAGTGGAAATCAGAAGATGTTGTATTAC
```

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**TITI E**

56

[illegible]

961 ACATGCTCCCTAGAGTCAATACTCTTGCATTTTCCCCCTCCTGCTCGGGGGGAAAAAGGT

**To Page No.**



177N

a T C S L E S I L L H F P P P A R G E K G -

1021 TGACATTTCCTGGCCCATTTCTCTCAGCTTGGTTTGTGTTGAATTGATGCTTGTGGAATG  
-----+-----+-----+-----+ 1080  
ACTGTAAAGACCGGGTAAAGGAAGAGTGAACCAAACAACTTAACCTACGAACACCTTAC

INTRON>

INTRON>

a \* H F W P I S F S A W F V \* I D A C G M -

1081 GIATTTTCATTACTTTAAGAGTGAAGATCCATAGTGAATTTGGATGGATGGTTGAATTAGA  
-----+-----+-----+-----+ 1140  
CATAAAGTAATGAAATTCTCACTTCTAGGATCACTTTAACCTACCTACCAACTTAATCT

a V F H Y F K S E D P \* \* N W M D G \* I R -

HindIII

1141 CGACCATTAAAGCTTACGTACGGC  
-----+-----+----- 1163  
GCTGGTAATTGCAATGCATGCGC

a R P L S L R T -

Enzymes that do cut:

HindIII

Untitled-5	MTLKYLWLVA LVALYISPIQ SQNCVYLDHT ILE	LRH	MSNS	VE	17				
Untitled-3	MTLKYLWLVA LVALYISPIQ SQNCVYLDHT ILE	MKI	IRTT	LR	50				
Consensus	.....				50				
Untitled-5	RNLIA	SC	TPM	KAF	EM	LO	FM	QHTFKYWKER	66
Untitled-3	KLITL	SC	TPM	KAF	EM	LO	FM	KDSISLATSE	100
Consensus	.....								100
Untitled-5	H K Q Q I D D Q A E Y L N Q L E								116
Untitled-3	R E R R S F K V Q Q A R E M V								146
Consensus	.....								150
Untitled-5	R R R R R R R R R R R R R R R R								164
Untitled-3	R R R R R R R R R R R R R R R R								191
Consensus	.....								198

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Page No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79																						

IFN

Project No. \_\_\_\_\_

Book No. \_\_\_\_\_

59

E

Ratio: 2.484

Gaps: 4

Percent Similarity: 63.383

Percent Identity: 63.383

Match display thresholds for the alignment(s):

| = IDENTITY

: = 5

. = 1

9808902.Con x Mrpe3-00078-F6-Wz.Ctg [REDACTED] 13:52 ..

1152 CACCTGGCAAATCTGAGACATCTGAGTAGTATGAGCAATTCATTTCCTG 1103

|| || | |||| | | | | | | | | | | | | | | | |

159 CATCTTGGAAAACATGAACTTCTGAGCAGCATCAGGACCACCTTTCCCT 208

1102 TAGAATGTCTACGAGAAAACATAGCTTTTGAGTTGCCCAAGAGTTTCTG 1053

|| || || || | | | | | | | | | | | | | | | |

209 TAAGATGTCTAAAGATATCACGGATTTTGAGTTTCTCAAGAGATTCTG 258

1052 CAATACACCCCAACCTATGAAGAGGGACATCAAGAAGGCCTTCTATGAAT 1003

| || | || | | | | | | | | | | | | | | | |

259 CTGTACGTCCAGCATGTGAAAAAGGACATAAAGGCAGTCACCTATCATAT 308

1002 GTCCCTACAGGCCTTCAACATCTTCAGCC...AACACACCTTCAAATATT 956

|| | | | | | | | | | | | | | | | | | |

309 ATCTTCTCTGGCGCTAATTATTTTCAGTCTTAAAGACTCCATCTCCCTGG 358

955 GGAAAGAGAGACACCTCAAACAAATCCAAATAGGACTTGATCAGCAAGCA 906

|| || | | | | | | | | | | | | | | | |

359 CGACAGAGGAACGCTTGAACGATATCAGATCGGGACTTTTCAAACAAGTG 408

905 GAGTACCTGAACCAATGCTTGGAGGAAGACGAGAATGAAAATGAAGACAT 856

|| | | | | | | | | | | | | | | | |

409 CAGCAAGCTCGAGAGTGCATGGTAGACGAGGAGAACAAGA.....ACAC 452

855 GAAAGAAATGAAAGAGAATGAGATGAAACCTCAGAAGCCAG.GGTCCCC 807

| | | | | | | | | | | | | | | | | |

453 GGAGG.....AGCAGATACATCAACATCCTCACTCAGAGGGCTTC 495

806 CAGCTGAGCAGCCTGGAACCTGAGGAGATATTTCCACAGGATAGACAATTT 757

|| | | | | | | | | | | | | | | | |

496 AAGGCAGTCTACCTGGAATTGAACAAGTATTTCTTCAGAATCAGAAAGTT 545

756 CCTGAAAGAAAAGAAATACAGTACTGTGCCTGGGAGATTGTCCGAGTGG 707

|||| | | | | | | | | | | | | | | | |

546 CCTGGTAAATAAGAAATACAGTTTCTGTGCCTGGAAGATTGTCTGGTGG 595

706 AAATCAGAAGATGTTTGTATTACTTTTACAAATT 673

|||| | | | | | | | | | | | | | | | |

596 AAATAAGAAGATGTTTCAGTATATTTTACAAACT 629

To Page No. \_\_\_\_\_

nessed & Understood by me,

Date

Invented by

Date



IFN

Rabbit α IFN

Programme	Interferon Like Protein			
Investigator:	Duanzhi Wen			
Animal/Quant	3 rabbits			
Immunogen:	Interferon like Protein			
Protocol:	MSU Standard			
Prog start date:				
Prog end date:	Ongoing			
Comments:	Give all sera to Duanzhi.			
ANIMAL# PI		50% Titer		50% Titer
#3429 5mls	30mls		30mls	
3432 5mls	30mls		30mls	
#3433 5mls	30mls		30mls	

Programme	Interferon Like Protein			
Investigator:	Duanzhi Wen			
Animal/Quant	3 rabbits			
Immunogen:	Interferon like Protein			
Protocol:	MSU Standard			
Prog start date:				
Prog end date:	Ongoing			
Comments:	Give all sera to Duanzhi.			
ANIMAL# PI		50% Titer		50% Titer
3429 5mls	30mls	1 1500	30mls	1 2000
3432 5mls	30mls	1 2500	30mls	1 3000
3433 5mls	30mls	1 5000	30mls	1 10,000
	50% Titer			
25mls	> 1 10,000			
25mls	> 1 10,000			
25mls	> 1 10,000			

**To Page**



AGGGAGAGGCAGAAGAAGATAAGAGAGAACGAGAAAAGACACCGGTAAACTTTCTCGAA

TGCTATATATACCACCTGIGGACTTCACCAAGACAATGGCTAGAGGATAGGGAGCAGAGA

1501 -----+-----+-----+-----+-----+ 1560

ACGATATATATGGTGGACACCTGAAGTGGTTCGTACCGATCTCCATCCCTCGTCTCT

ATGTTGCAAATGGTAACATTTCAATGACTTAACTGTTTTGCTGCCAAGGTTCCTTATCC

1561 -----+-----+-----+-----+-----+ 1620

TACAACGTTTTACCATTGTAAAGTTACTGAATTGACAAAACGACGGTTCACCAACGAATAGG

TATGAAAATTCAGCACATTAAAAGAGCTTATACATGCTCCCTAGAGTCAATACTCTTGCA

1621 -----+-----+-----+-----+-----+ 1680

ATACTTTTAAGTCGTGTAATTTTCTCGAATATGTACGAGGGATCTCAGTTATGAGAACGT

TTTTCCCCCTCCTGCTCGGGGGGAAAAGGTTGACATTTCTGGCCCATTTCCCTTCTCAGC

1681 -----+-----+-----+-----+-----+ 1740

AAAAGGGGAGGACGAGCCCCCTTTTTCCAACGTAAAGACCGGGTAAAGGAAGAGTCG

TIGGTTTGTTTGAATTGATGCTTGIGGAATGGIATTTCACTTTAAGAGTGAAGATCC

1741 -----+-----+-----+-----+-----+ 1800

AACCAAACAACTTAACTACGAACACCTTACCATAAAGTAATGAAATTCTCACTTCTAGG

HindIII

ATAGTGAAATTGGATGGATGGTTGAATTAGACGACCATTAAAGCTTGGATCCTCTAGAGCG

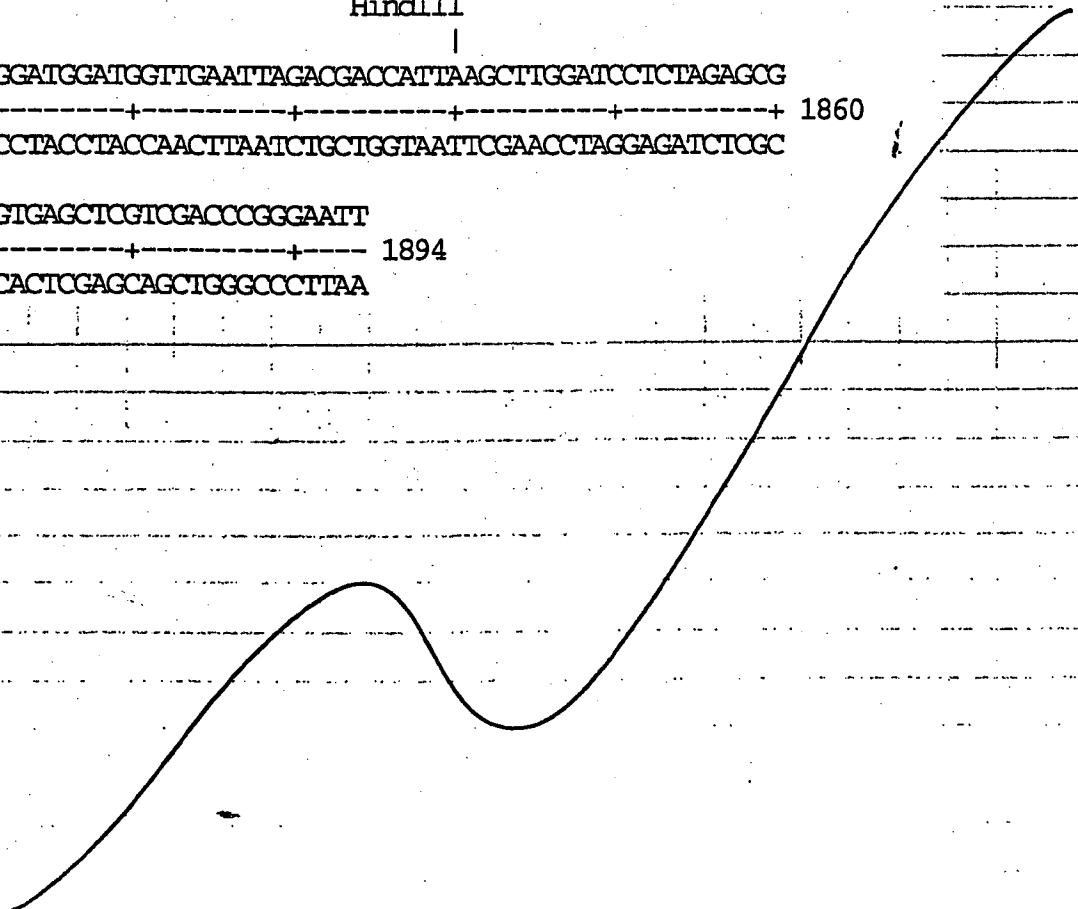
1801 -----+-----+-----+-----+-----+ 1860

TATCACTTTAACCTACCTACCAACTTAATCTGCTGGTAATTGAACTTAGGAGATCTCGC

GCGCGCGACTAGTGAGCTCGTCGACCCGGGAATT

1861 -----+-----+-----+-----+ 1894

CGCGCGCTGATCACTCGAGCAGCTGGGCCCCTTAA





## 65

[illegible]

To Page No.

Project No. \_\_\_\_\_

Book No. \_\_\_\_\_

TITLE \_\_\_\_\_

27N

66

rat clone

10 30 50  
GTCGACCCACGCGTCCGGGGTGTGTAGATATTTTTCCTTTGGAAGAAATACTGAGCACC  
70 90 110  
AAGGCTGAGATGACACTGAAGTATTTATGGCTGGTGGCCCTCGTGGCTCTATACATTTCA  
MetThrLeuLysTyrLeuTrpLeuValAlaLeuValAlaLeuTyrIleSer  
130 150 170  
CCCATCCAGTCTCAGAACTGTGTGTATCTGGATCATACCATCTTGAAAACATGAACTT  
ProIleGlnSerGlnAsnCysValTyrLeuAspHisThrIleLeuGluAsnMetLysLeu  
190 210 230  
CTGAGCAGCATCAGGACCACCTTTCCCTTAAGATGTCTAAAAGATATCACGGATTTTGAG  
LeuSerSerIleArgThrThrPheProLeuArgCysLeuLysAspIleThrAspPheGlu  
250 270 290  
TTTCTCAAGAGATTCTGCTGTACGTCCAGCATGTGAAAAAGGACATAAAGGCAGTCACC  
PheProGlnGluIleLeuLeuTyrValGlnHisValLysLysAspIleLysAlaValThr  
310 330 350  
TATCATATATCTTCTCTGGCGCTAATTATTTTTCAGTCTTAAAGACTCCATCTCCCTGGCG  
TyrHisIleSerSerLeuAlaLeuIleIlePheSerLeuLysAspSerIleSerLeuAla  
370 390 410  
ACAGAGGAACGCTTGGAACGTATCAGATCGGGACTTTTICAAACAAGTGCAGCAAGCTCGA  
ThrGluGluArgLeuGluArgIleArgSerGlyLeuPheLysGlnValGlnGlnAlaArg  
430 450 470  
GAGTGCATGGTAGACGAGGAGAACAAGAACACGGAGGAGCAGTACATCACAACTCTCT  
GluCysMetValAspGluGluAsnLysAsnThrGluGluAspSerThrSerGlnHisPro  
490 510 530  
CACTCAGAGGGCTTCAAGGCAGTCTACCTGGAATTGAACAAGTATTTCTTTCAGAATCAGA  
HisSerGluGlyPheLysAlaValTyrLeuGluLeuAsnLysTyrPhePheArgIleArg  
550 570 590  
AAGTTCCTGGTAAATAAGAAATACAGTTTCTGTGCTGGAAGATTGTCTGGTGGTGAATA  
LysPheLeuValAsnLysLysTyrSerPheCysAlaTrpLysIleValValValGluIle  
610 630 650  
AGAAGATGTTTCAGTATATTTTACAACTACTCAACATGAATTGAGAATCATCCAGCTTC  
ArgArgCysPheSerIlePheTyrLysLeuLeuAsnMetAsnEnd  
670 690 710  
AAGCAAGAACTTAGATAGAAGTTGTGACTGCTCAAATGTCCCCAAGAACGCTTGATTCTA  
730 750 770  
AGGCTATTGCGAGTCTGCTGCTACACACTTCGGACGCAAGACTTTTCAAGGTCAGGGTTC  
790 810 830  
AAGGCAGTACAGTCAAAGGAAGTCTTATGTTAAGCAAAAGAAAAATTTTCAGTGGAAAAGC  
850 870 890  
TAGCAGAAATGTCAACTGTCAAAAAACAACCTTATGGATTATGGCATTGACGTTACTAG  
910 930 950  
CAAAAAAATAAAACAAAAAACAACAGTCACTAAAAAAGGGCGGC

CGC

# Nucleotide comparison

WChen

DNA=hgmrep3-6.2

assembled by JK

9808903.con

JFN

to: Mrpe3-00078-F6-Wz.Ctg check: 4485 from: 1 to: 963

From: INTRON::DONGYINY 16:07:43.44

To: WCHEN

CC:

Subj:

From: INTRON::JCAO 12:24:38.19

To: DONGYINY . . .

Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Swgapdna.Cmp  
CompCheck: 2335

Gap Weight: 50 Average Match: 10.000  
Length Weight: 3 Average Mismatch: -9.000

Quality: 1457 Length: 634  
Ratio: 2.392 Gaps: 6  
Percent Similarity: 63.516 Percent Identity: 63.516

Match display thresholds for the alignment(s):

| = IDENTITY

: = 5

, = 1

9808903.Rev x Mrpe3-00078-F6-Wz.Ctg 15:04 ..

555 TCTTCTGGATTTTTTTAGCTT..GCAAAAAAATGAGCACCAACCTGATA 602

| | | | | | | | | | | | | | | | | | | | | | | | | | | |

21 TGTTGTAGATATTTTTCCTTTGGAAGAAATACTGAGCACCAAGGCTGAGA 70

603 TGATTCAAAAGIGTTTGGGCTTGAGATCCTTATGGGTATATTTCATTGCT 652

| | | | | | | | | | | | | | | | | | | | | | | | | | | |

71 TGACACTGAAGTATTTATGGCTGGTGGCCCTGGTGGCTCTATACATTICA 120

653 GGCACCCCTATCCCTGGACTGTAACTTACTGAACGTTCAACCTGAGAAGAGT 702

| | | | | | | | | | | | | | | | | | | | | | | | | | | |

121 CCCATCCAGTCTCAGAACTGT.....GTGTATCTGGATCATAC 158

703 CACCTGGCAAAATCTGAGACATCTGAGTAGTATGAGCAATTCATTTCCCTG 752

| | | | | | | | | | | | | | | | | | | | | | | | | | | |

159 CATCTTGGAAAACATGAACTTCTGAGCAGCATCAGGACCACCTTTCCCT 208

753 TAGAATGICTACGAGAAAACATAGCTTTTGAGTTGCCCAAGAGTTTCTG 802

| | | | | | | | | | | | | | | | | | | | | | | | | | | |

209 TAAGATGICTAAAAGATATCAGGATTTTGAGTTTCCCTCAAGAGATTCTG 258

803 CAATACACCCAACCTATGAAGAGGGACATCAAGAAGGCCTTCTATGAAAT 852

| | | | | | | | | | | | | | | | | | | | | | | | | | | |

259 CTGTACGTCAGCATGTGAAAAAGGACATAAAGGCAGTCACCTATCATAT 308

853 GTCCTACAGGCCTTCAACATCTTCAGCC...AACACACCTTCAAAATATT 899  
 || ||| || || ||||| || ||| |||  
 309 ATCTTCTCTGGCGCTAAATTATTTTCAGTCTTAAAGACTCCATCTCCCTGG 358  
 900 GGAAAGAGAGACACCTCAAACAAATCCAAATAGGACTTIGATCAGCAAGCA 949  
 || |||| || | || ||| || | ||||| | ||||  
 359 CGACAGAGGAACGCTTGGAACGTATCAGATCGGGACTTTTCAAACAAGTG 408  
 950 GAGTACCTGAACCAATGCTTGGAGGAAGACGAGAATGAAATGAACACAT 999  
 || | ||| ||| || ||||| || |||  
 409 CAGCAAGCTCGAGAGTGCATGGTAGACGAGGAGAACAAGA.....ACAC 452  
 1000 GAAAGAAATGAAAGAGAATGAGATGAAACCTCAGAGCCAG.GGTCCCC 1048  
 || | || ||| ||| ||| ||| ||| ||| ||| |||  
 453 GGAGG.....AGGACAGTACATCACAACATCCTCACTCAGAGGGCTTC 495  
 1049 CAGCTGAGCAGCCTGGAAGTGGAGATATTTCCACAGGATAGACAATTT 1098  
 || | ||||| ||| | ||||| ||| || |||  
 496 AAGGCAGTCTACCTGGAATTGAACAAGTATTTCTTCAGAATCAGAAAGTT 545  
 1099 CCTGAAAGAAAAGAAATACAGTACTGTGCTGGGAGATTGTCCGAGTGG 1148  
 |||| | ||||| ||||| ||||| ||||| ||||| |||||  
 546 CCTGGTAAATAAGAAATACAGTTTCTGCTGGAGATGTGCTGGTGG 595  
 1149 AAATCAGAAGATGTTTGTATTACTTTTACAAATT 1182  
 |||| ||||| || | ||||| |||  
 596 AAATAAGAAGATGTTTCAGTATATTTTACAAACT 629

ITN

Project No. \_\_\_\_\_

Book No. \_\_\_\_\_

protein sequence comp

BESTFIT of: 9808903.Pep check: 4904 from: 1 to: 201

TRANSLATE of: 9808903.rev check: 8672 from: 602 to: 1205  
generated symbols 1 to: 201.

REVERSE-COMPLEMENT of: 9808903.Con check: 57 from: 1 to: 1894  
When  
DNA-hgmrep3-6.2  
assembled by JK: [REDACTED] . . .

to: Mrpe3-00078-F6-Wz.Pep check: 5990 from: 1 to: 192

TRANSLATE of: mrpe3-00078-f6-wz.ctg check: 4485 from: 70 to: 646  
generated symbols 1 to: 192.

From: INTRON::DONGYINY [REDACTED] 16:07:43.44

To: WCHEN

CC:

Subj: . . .

Symbol comparison table: Gencoredisk: [Gcgcore.Data.Rundata]Blosum62.Cmp  
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912  
Length Weight: 4 Average Mismatch: -2.003

Quality: 292 Length: 194  
Ratio: 1.570 Gaps: 3  
Percent Similarity: 49.730 Percent Identity: 40.541

Match display thresholds for the alignment(s):

| = IDENTITY

: = 2

. = 1

9808903.Pep x Mrpe3-00078-F6-Wz.Pep [REDACTED] 14:55 ...

1 MIQKCLWLEILMGIFIAGTILSLDCNLLNVHLRRVTWQNLRLSSMSNSFP 50

| | | | | . : : | . | | : | : : | | | . | |

1 MILKYLWLVALVALYISPIQSONC....VYLDHTLENMKLLSSIRITFP 46

51 VECLRENTAFELPQEFLOYTOPMKRDIKKAFYEMSLQAFNIFS.QHIFKY 99

. | | : : | | | | | | . : | | | | | . | | | | .

47 LRCLKDITDFEFQEIILLYVQHVKKDIKAVTYHISSLALITIFSLKDSISL 96

100 WKERHLKQIQIGLDQQAIEYLNOCLEEDENENEDMKEMKENEMKPSEARVP 149

| | . . | | . | : : | : : | | . | : : .

97 ATEERLERIRSGLFKQVQQAECMVDEENKNTIEDSTSQPHSEGFKAV. 145

150 QLSSLELRRYFHRIDNFLKEKKYSDCAWEIVRVEIRRLYYFYK 193

| | | : | | | | | | | | | | | | | | | | |

146 ...YLELNKYFFRIRKFLVNKKYSFCWIKIVVVEIRRCFSIFYK 186

To Page No. \_\_\_\_\_

nessed & Understood by me,

Date

Invented by

0

Date

50

100

150

200

231

17% idem

4.

85

122

157

187

•

1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

71  
6/1/98  
IFN

NotI  
EagI  
EaeI  
HhaI  
HinPI  
BsiEI  
BanII

Factor 2A  
Factor 2A  
Factor 2A  
Factor 2A  
Factor 2A  
Factor 2A  
Factor 2A

10 20 30 40 50 60 70 80 90 100

1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

NotI  
EagI  
EaeI  
HhaI  
HinPI  
BsiEI  
BanII

Factor 2A  
Factor 2A  
Factor 2A  
Factor 2A  
Factor 2A  
Factor 2A  
Factor 2A

10 20 30 40 50 60 70 80 90 100

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NotI  
EagI  
EaeI  
HhaI  
HinPI  
BsiEI  
BanII

Factor 2A  
Factor 2A  
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Factor 2A  
Factor 2A  
Factor 2A

10 20 30 40 50 60 70 80 90 100

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NotI  
EagI  
EaeI  
HhaI  
HinPI  
BsiEI  
BanII

Factor 2A  
Factor 2A  
Factor 2A  
Factor 2A  
Factor 2A  
Factor 2A  
Factor 2A

10 20 30 40 50 60 70 80 90 100

1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

Oligo No.: 1954-45  
Researcher: when  
Purification: FOP  
Standard Order

Sequence  
ACG CGT CGA CTT ATT ATT TCC TCC TGA ATA G  
Display Expanded Sequence  
Sal I + 2x stop codon (stop positive)

Oligo No.: 1954-46  
Researcher: when  
Purification: FOP  
Standard Order

Sequence  
AAG GAA AAA AGC GGC CGC TTA TTA TTT CCT CCT  
GAA TAG AGC  
Display Expanded Sequence  
Not I + 2x stop codon (stop positive)

Oligo No.: 1954-47  
Researcher: when  
Purification: FOP  
Standard Order

Sequence  
CCC AAG CTT ACC ATG ATT CAA AAG TGT TIG TGG  
Display Expanded Sequence  
Hind III + ATG @ 5'

Oligo No.: 1954-48  
Researcher: when  
Purification: FOP  
Standard Order

Sequence  
AAG GAA AAA AGC GGC CGC GGC GGC CTC GAT TT  
CCT CCT GAA TAG AGC TGT AA  
Display Expanded Sequence  
Not I + 2x stop codon (stop positive)

Oligo No.: 1954-49  
Researcher: when  
Purification: FOP  
Standard Order

Sequence  
AAG GAA AAA AGC GGC CGC TTT CCT CCT GAA TAG  
AGC TGT AA  
Display Expanded Sequence  
Not I

JFN

From Page No. \_\_\_\_\_

**Chen, Wen**

From: Schultz, Henry  
Sent: Friday, [REDACTED] 5:15 PM  
To: Chen, Wen  
Subject: RE: human interferon like seq.

Wen - the human predicts cytokine strongly  
scoreaaccomp= -2.9 scoredipep= 19 ACCEPT (Probability 91%).

The human is predicted to be signal peptide as follows:

MIQKCLWLEILMGIFIAGTL\$ cleavage LD.....etc

For the rat, the cytokine prediction is lost but the signal peptide is:

MTLKYLWLVALVALYISPIQS cleavage QN....etc

Henry

-----  
From: Chen, Wen  
Sent: Friday, [REDACTED] 4:02 PM  
To: Schultz, Henry  
Subject: human interferon like seq.

Henry: please help me look at the signal peptide for the human clone sequence.  
Thanks.

Wen Chen

Human sequence:

MIQKCLWLEILMGIFIAGTL SLDCNLLNVH LRRVTWQNLRL HLSSMSNSFP

51 VECLRENIAF ELPQEFLQYT QPMKRDIKKA FYEMSLQAFN IFSQHTFKYW

101 KERHLKQIQI GLDQQAAYLN QCLEEDENEN EDMKEMKENE MKPSEARVPQ

151 LSSLELRRYF HRIDNFLKEK KYSDCAWEIV RVEIRRCLYY FYKFTALFRR

201 K

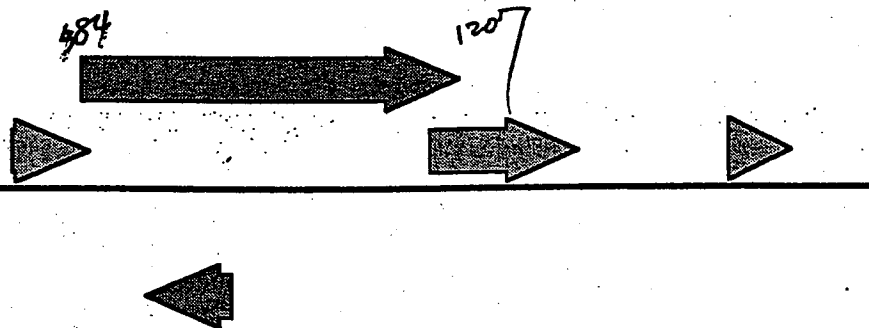




1890  
GCGGCCGACTAGTGAGCTCGTCGACCCGGGAATT

12000

Frame -3



One more ATG @ 684 in frame with ATG starting from 602.

# RESEARCH SUMMARY PAGE

01067  
McDonnell  
GN-0001

## Gene Name:

## All Known Alias Gene Names:

Human: Zhwxc00-00001-a1  
Rat: Agp-22423-a1

Member of the interferon family of proteins  
Name: Interferon-like protein.

## Investigator(s):

## Initial Date of Summary Preparation:

Duanzhi Wen, Andrew Welcher, Michael  
Kelley

Initial invention disclosure filed [REDACTED]  
This summary filled in on [REDACTED]

## Description of Project:

This novel member of the interferon family of proteins is related to the beta, alpha, and omega subfamilies. As an interferon it would be expected to have anti-infective and anti-proliferative uses. Additionally, it might find use in the treatment of multiple sclerosis and other pathologies requiring immunomodulation.

## Gene Nucleotide Sequence:

### Human:

```
1  CGCGTACGTA AGCTTAATTT AACAAAATTG GAAAAACCTA AACTATACTG
51  TGCTCTGGTG ACCTAGCAAT CAAATAATCA CAGTCATTG GTCAATGTCT
101 ATGATTAACCT CAATGAGACA GGATGTTTGG CTATAGCACC AGGTACAAAA
151 AATATATTTT CATGAAGGAT CACTCCCTCT TATGTAATAG ATTTGGGTGA
201 GTGAGTGAGT GAGTGAGTGC ATGGACTCAC AGCTTTTGGC TTTCTGAAAT
251 ACCCTGCATC AGTCTTGTTA TGATGATTCC TTAGTGCTGG GATGGATCAT
301 CCAGGCATTT AAGGTAACAC GATGGTAATT CTTTGCTCAT TTTTCAGGGA
351 AAAAAAAAG TTATCACTTC CAAAGTCGGC ATAGTCACCC GAAGTAAAAA
401 AAAAAAAAG AAAAAAAGC CTCAGAGGCA AAGGAAAGGG GCCGCAACCT
451 TGGTAACTG TGAAATGACG AATGAGAAAA CTCCTCCTGC TGAAGATATT
501 CAGGTATATA AAGGCACATG AAGGAAAACT CAAAACATCA TTGTCATATA
551 CACATCTTCT GGATTTTTTA GCTTGCAAAA AAAATGAGCA CCAAACCTGA
601 TATGATTCAA AAGTGTGTTG GGCTTGAGAT CCTTATGGGT ATATTCAATTG
651 CTGGCACCTT ATCCCTGGAC TGTAACCTAC TGAACGTTCA CCTGAGAAGA
701 GTCACCTGGC AAAATCTGAG ACATCTGAGT AGTATGAGCA ATTCATTTC
751 TGTAGAATGT CTACGAGAAA ACATAGCTTT TGAGTTGCCC CAAGAGTTTC
801 TGCAATACAC CCAACCTATG AAGAGGGACA TCAAGAAGGC CTTCTATGAA
851 ATGTCCTTAC AGGCCTTCAA CATCTTCAGC CAACACACCT TCAAATATTG
901 GAAAGAGAGA CACCTCAAAC AAATCCAAAT AGGACTTGAT CAGCAAGCAG
951 AGTACCTGAA CCAATGCTTG GAGGAAGACG AGAATGAAAA TGAAGACATG
1001 AAAGAAATGA AAGAGAATGA GATGAAACCC TCAGAAGCCA GGGTCCCCCA
1051 GCTGAGCAGC CTGGAACCTG GGAGATATTT CCACAGGATA GACAATTTCC
1101 TGAAGAGAAA GAAATACAGT GACTGTGCCT GGGAGATTGT CCGAGTGGAA
1151 ATCAGAAGAT GTTTGTATTA CTTTACAAA TTTACAGCTC TATTCAGGAG
1201 GAAATAAGGT ATATTTTTGG AATTAAATTT CCTTTTCCCT CCGAAATCTC
1251 TTTCTCCTTC TCCTCCTCCA TCTTCTTTT AAGGATTGTT GTGCTGTCTC
1301 GTAAGCCTGT CCTCAGTTGG ACTGGTAGCC TCGGAACATC AGGGACACTC
```

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1351 ACCTCTCTAA GGAGAGGTAA TGCCAACCAT CCTCAGGGTG ACCAAGAGTC
1401 TCCTTAGAAA GTCTTTAAGA CATTTTTAAA GGAATAAGAT TCCCTCTCCG
1451 TCTTCTCTA TTCTCTCTTG CTCTTTTCTG TGGCCATTTT GAAAGAGCTT
1501 TGCTATATAT ACCACCTGTG GACTTCACCA AGACAATGGC TAGAGGATAG
1551 GGAGCAGAGA ATGTTGCAAA ATGGTAACAT TTCAATGACT TAACTGTTTT
1601 GCTGCCAAGG TTGCTTATCC TATGAAAATT CAGCACATTA AAAGAGCTTA
1651 TACATGCTCC CTAGAGTCAA TACTCTTGCA TTTTCCCCCT CCTGCTCGGG
1701 GGGAAAAAGG TTGACATTTT TGGCCCATTT CCTTCTCAGC TTGGTTTGTT
1751 TGAATTGATG CTTGTGGAAT GGTATTTTCA TACTTTAAGA GTGAAGATCC
1801 ATAGTGAAAT TGGATGGATG GTTGAATTAG ACGACCATTA AGCTTGGATC
1851 CTCTAGAGCG GCCGCCGACT AGTGAGCTCG TCGACCCGGG AATT

```

Rat:

```

1 GGGTGTGTA GATATTTTTC CTTTGGAAGA AATACTGAGC ACCAAGGCTG
51 AGATGACACT GAAGTATTTA TGGCTGGTGG CCCTCGTGGC TCTATACATT
101 TCACCCATCC AGTCTCAGAA CTGTGTGTAT CTGGATCATA CCATCTTGGA
151 AAACATGAAA CTTCTGAGCA GCATCAGGAC CACCTTTCCC TTAAGATGTC
201 TAAAAGATAT CACGGATTTT GAGTTTCCTC AAGAGATTCT GCTGTACGTC
251 CAGCATGTGA AAAAGGACAT AAAGGCAGTC ACCTATCATA TATCTTCTCT
301 GGCGCTAATT ATTTTCAGTC TTAAAGACTC CATCTCCCTG GCGACAGAGG
351 AACGCTTGGA ACGTATCAGA TCGGGACTTT TCAAACAAGT GCAGCAAGCT
401 CGAGAGTGCA TGGTAGACGA GGAGAACAAG AACACGGAGG AGGACAGTAC
451 ATCACAACAT CCTCACTCAG AGGGCTTCAA GGCAGTCTAC CTGGAATTGA
501 ACAAGTATTT CTTCAGAATC AGAAAGTTCC TGGTAAATAA GAAATACAGT
551 TTCTGTGCCT GGAAGATTGT CGTGGTGGAA ATAAGAAGAT GTTTCAGTAT
601 ATTTTACAAA CTAATCAACA TGAATTGAGA ATCATCCAGC TTCAAGCAAG
651 AACTTAGATA GAAGTTGTGA CTGCTCAAAT GTCCCCAAGA ACGCTTGATT
701 CTAAGGCTAT TGCGAGTCTG CTGCTACACA CTTCCGACGC AAGACTTTTC
751 AAGGTCAGGG TTCAAGGTAG TACAGTCAAA GGAAGTCTTA TGTTAAGCAA
801 AAGAAAAATT TCAGTGGAAA AGCTAGCAGA AATGTCAACT TGTCAAAAAA
851 ACAACTTATG GATTATGGCA TTGACGTTAC TAGCAAAAAA AATAAAACAA
901 AAAAAAACAA AAA

```

### Gene Amino Acid Sequence:

Human:

```

1 MSTKPDMIQK CLWLEILMGI FIAGTSLSDC NLLNVHLRRV TWQNLRLHLS
51 MSNSFPVECL RENIAFELPQ EFLQYTQPMK RDIKKAFYEM SLQAFNIFSQ
101 HTFKYWKERH LKQIQIGLDQ QAEYLNQCLE EDENENEDMK EMKENEMKPS
151 EARVPQLSSL ELRRYPFHRID NFLKEKKYSYD CAWEIVRVEI RRCLYYPYKF
201 TALFRRK*

```

Rat:

```

1 MTLKYLWLV LVALYISPIQ SQNCVYLDHT ILENMKLLSS IRTTFPLRCL
51 KDITDFEFPQ EILLYVQHV KDIKAVTYHI SSLALIIFSL KDSISLATEE
101 RLERIRSGLF KQVQQAECM VDEENKNTTE DSTSQHPHSE GFKAVYLELN
151 KYFFRIRKFL VNKKYSFCAW KIVVVEIRRC FSIFYKLLNM N*

```

### Figure Containing cDNA and Amino Acid Sequences:

Human:

# Sequence Analysis of Human IFN-novel

1	CCGCTACGTAAGCTTAATTTAAACAAAATTGGAAAAACCTAAACTATCTGTCTGTGGTG	60
61	ACCTAGCAATCAAAATAATCACTCATTTTGGTCAATGCTTACGATTAAGTCAATGAGACA	120
121	CGATCTTTGGCTATAGCACCACCTACAAAATAATATTTTCATCAAGGATCACTGGCTGT	180
181	TATCTAATAGATTTGGGTGACTCACTGAGTGAAGTGCATGCACTCACAGCTTTTGGG	240
241	TTTCTGAAATAGCTTGCATCACTCTTTTATGATGATTCCTTACTGCTGGCATGATCAT	300
301	CCAGGATTTTAAGGTAAACCAATGTAATTTCTTCTCATTTTTCAGGAAAAAAAAG	360
361	TTATCACTTCCAAAGTCCCACTACTCACCGGAAGTAAAAAAAATAAAAAAAGG	420
421	CTCAGCGCCAAAGGAAAGCCGCCCAACCTTCTTAACTGTGAAATCAGCAATCAAAA	480
481	CTCTCTCTCTCAAGATATTACGTTATATAAACCCACATGAAGCAAACTCAAAACATCA	540
541	TTGTCAATACACATCTTCTGGATTTTTCAGCTTCCAAAATAATGAGCACCAACCTGA	600
601	TATGATTCAAAATGTTTGTGCTTGCATCTTAAGGATATATTCATTTCTGCTGCCACCT	660
1	<u>MTDFCLWLEFLINQTFAGTL</u>	70
661	ATCCCTGCACTGTAACTTACTGAAAGCTTCACTCAGAGAGTCACTTCCAAAATCTCAG	720
721	<u>SDCNLLNVHLRVRTWONLR</u>	780
781	ACATCTGACTAGTATGAGCAATTCATTTCTCTGACAAATGTTAGGCAAAACATAGCTTT	840
841	CTTCTATGAAATGCTGTACAGCCCTTCAACATCTTCAGGCAAGCAGACCTTCAAAATG	900
901	FTYEMSLQAVMIFSQHTFVFW	960
961	GAAAGAGAGACCTCAACCAATGCCAAATAGCACTTCATGAGCAAGCAGAGTACCTGAA	1020
1021	KEARHLEQIQIGLDQQAERYLN	1080
1081	CGATGCGAAATGCAAGCAATGTAATGCAACATCAAGCAATGGAAGCAATGCA	1140
1141	QCLREDEHNSNDMEKKNKNS	1200
1201	GATGAAACCTTCAGAACCCAGCTGCGGAGCTGACGAGCTGCAACTGAGGATATTT	1260
1261	MKFSBARVPQLSSLELRYP	1320
1321	CCACAGGATACCAATTTCTGTAAGAAAGAAATACAGTCACTGCTGCTGGAGATTTG	1380
1381	HREDFLEKEKYSDCAMSEIV	1440
1441	CGAGTGGAAATCAGAACATTTGTATTAGTTTACAAATTAACCTGCTATTGAGGAG	1500
1501	RVERIRCLYYPYKPTALFER	1560
1561	GAAATAGGATATTTTTCGAATTAATTTCTTTTCCCTCCGAAATCTCTTCTGCTTC	1620
1621	K	1680
1681	TCCCTTCGATTTCTTTTAAAGCATCTCTCTCTCTCTCTGTAAGCCTCTCTCTCTCTG	1740
1741	ACTGTAAGCTTGGATCATGAGGACACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1800
1801	CT	1860
1861	TCCCT	1920
1921	ATGTTGCAAAATCTTAAGATTTCAATGACTTAACTGTTTCTCTCTCTCTCTCTCTCT	1980
1981	TATGAAATTCAGCACATTAAGAGCTTATACATCTCTCTCTCTCTCTCTCTCTCTCT	2040
2041	TTTTCCT	2100
2101	TTGTTTGTGAAATTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2160
2161	ATAGTAAATTCGATGCAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2220
2221	GCGCGGAGTACTGACCT	2280
2281	ATGTTGCAAAATCTTAAGATTTCAATGACTTAACTGTTTCTCTCTCTCTCTCTCTCT	2340
2341	TATGAAATTCAGCACATTAAGAGCTTATACATCTCTCTCTCTCTCTCTCTCTCTCT	2400
2401	TTTTCCT	2460
2461	TTGTTTGTGAAATTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2520
2521	ATAGTAAATTCGATGCAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2580
2581	GCGCGGAGTACTGACCT	2640
2641	ATGTTGCAAAATCTTAAGATTTCAATGACTTAACTGTTTCTCTCTCTCTCTCTCTCT	2700
2701	TATGAAATTCAGCACATTAAGAGCTTATACATCTCTCTCTCTCTCTCTCTCTCTCT	2760
2761	TTTTCCT	2820
2821	TTGTTTGTGAAATTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2880
2881	ATAGTAAATTCGATGCAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2940
2941	GCGCGGAGTACTGACCT	3000

A human gene which encodes a novel protein of 207 amino acids was isolated by screening the human genomic DNA library using a rat cDNA clone. The deduced amino acid sequence of this novel gene is indicated below the first nucleotide of each codon, and the termination codon is marked with an asterisk. The protein starts with cysteine, and the signal peptide is underlined. This novel protein is 27% identical to human IFN- $\beta$ .

Rat:

1	GGGTGTGTAGATATTTTCTCTTGGGAAGAAATACTGAGCACCAAGGCTGAGATGACACT	60
1	—	3
		M T L
61	GAAGTATTTATGGCTGGTGGCCCTCGTGGCTCTATACATTTACCCATCCAGTCTCAGAA	120
4	K Y L W L V A L V A L Y I S P I O S O N	23
121	CTGTGTGTATCTGGATCATACCATCTTGGAAAACATGAACTTCTGAGCAGCATCAGGAC	180
24	C V Y L D H T I L E N M K L L S S I R T	43
181	CACCTTTCCTTAAAGATGTCTAAAGATATCACGGATTTGAGTTTCTCAAGAGATTCT	240
44	T F P L R C L K D I T D F E F P Q E I L	63
241	GCTGTACGTCCAGCATGTGAAAAAGGACATAAAGGCAGTCACCTATCATATATCTTCTCT	300
64	L Y V Q H V K K D I R A V T Y H I S S L	83
301	GGCGCTAATTATTTTCAGTCTTAAAGACTCCATCTCCCTGGCGACAGAGGAACGCTTGA	360
84	A L I I F S L K D S I S L A T E E R L E	103
361	ACGTATCAGATCGGACTTTTCAACAAGTGCAGCAAGCTCGAGAGTGCATGGTAGACGA	420
104	R I R S G L F K Q V Q Q A R E C M V D E	123
421	GGAGAACAAGAACACGGAGGAGGACAGTACATCACAACTCCTCACTCAGAGGGCTTCAA	480
124	E N K N T E E D S T S Q H P H S E G F K	143
481	GGCAGTCTACCTGGAATTGAACAAGTATTTCTTCAGAATCAGAAAGTTCTGGTAAATAA	540
144	A V Y L E L N K Y F F R I R K F L V N K	163
541	GAAATACAGTTTCTGTGCTGGAAGATTGTGCTGCTGGAATAAGAAGATGTTTCAGTAT	600
164	K Y S F C A W K I V V V E I R R C F S I	183
601	ATTTTACAACTACTCAACATGAATTGAGAATCATCCAGCTTCAAGCAAGAACTTAGATA	660
184	F Y K L L N M N *	192
661	GAAGTTGTGACTGCTCAAATGTCCCAAGAAGCGCTTGATTCTAAGGCTATTGCGAGTCTG	720
721	CTGCTACACACTTCGGACGCAAGACTTTTCAAGGTCAAGGTTCAAGGCAGTACAGTCAAA	780
781	CGAAGTCTTATGTTAAGCAAAAGAAAAATTTCAAGTGGAAAAGCTAGCAGAAATGTCAACT	840
841	TGTCAAAAAACAACCTTATGCTTATGGCATTGACGTTACTAGCAAAAAAATAAAACAA	900
901	AAAAAACAACAGTCACTAAAA	923

### Cloning Information:

The rat sequence was cloned from a rat placenta cDNA library as part of an EST project and was identified by computer analysis as being a novel member of the interferon family of proteins. Briefly, rat embryo day 17 [E17] placenta mRNA was isolated by standard methods (unnecessary information) (Chomczynski, P. and Sacchi, N., Anal. Biochem. 162, 156, 1987). cDNA was synthesized using the SuperScript Plasmid cDNA kit supplied by GIBCO/BRL and subcloned into the pSPORT1 (GIBCO/BRL) vector into the Sal I and Not I restriction sites.

### Cloning of Human IFN-like gene:

Multiple attempts to clone the human IFN-like gene from a variety of human tissue cDNA libraries failed to yield positive clones. However, a human tissue Northern Blot

hybridized with a PCR-generated radioactive rat probe revealed an 1.8 kb Hind III fragment in certain batches of human pancreas mRNA. Attempts to clone this corresponding message in a pancreas cDNA library failed to recover any positive clones.

Examination of the genomic structures of known IFNs revealed that IFN, especially the members in the IFN $\alpha$  family, all share a unique intronless genomic structure. Therefore, screening of human genomic DNA might yield the complete human IFN-like gene. We started with  $1 \times 10^6$  human lambda genomic clones (Stratagene, Cat. No. 946206) for primary screening at a density of 50,000 clones / plate (*unnecessary information*). Nitrocellulose filters (*unnecessary information*) (S&S) were prepared by standard techniques (Molecular Cloning, A Laboratory Manual, Sambrook, Fritsch, and Maniatis editors).

The following conditions were used.

- Prehybridization and hybridization conditions: 30% formamide, 5x SSC, 2x Denhart's, 10 $\mu$ g/ml Salmon sperm DNA, 0.2% SDS, 2mM EDTA and 0.1% pyrophosphate. Hybridization was conducted overnight at 42°C. The washings were done under following conditions: 1x SSC, 0.1% SDS at room temperature for 30-60 minutes followed by 0.2x SSC and 0.1% SDS at 55°C for 15 minutes.
- Generation of radioactive PCR probe (*unnecessary information*): rat cDNA full-length fragment 20ng, primer 1795-01 and 1795-02, 20 pmol each, 1mmol dNTP (dCTP @ 0.01mmol), 32P-dCTP 5 ml and 4mM MgCl<sub>2</sub>. Reaction condition: denature at 94°C for 30sec, anneal at 60°C for 30sec and elongate at 72°C for 1 minute. The reaction is repeated for a total of 45 times. Simultaneously a "cold" PCR reaction is performed under exact condition except the dNTP mix is dCTP balanced. The radioactive probe was purified by Quick Spin G-50 column and boiled at 100°C for 10 minutes before chilling on dry ice for 20 minutes. The probe is usually  $5 \times 10^5$  cpm/ $\mu$ l.

Three positive clones were recovered after primary, secondary screening and subsequently purified to homogeneity. The lambda phage DNA was prepared by a solid plate culture method. The NotI insert from these clones were excised out and ligated into pSport (GIBCO BRL) vector and transformed into DH10 E. coli strain. The transformants were prepared by Qiagen Spin Column plasmid prep kit. The plasmid DNA was then digested with HindIII. The digested fragments were resolved on agarose gel and transferred to a nylon membrane for Southern Blot analysis. The analysis was conducted under the same condition genomic screening was carried out. The corresponding fragment recognized by "hot" rat probe was then subcloned in pSport vector for sequencing analysis. According to the HindIII digestion pattern, we determined these three independent clones were likely to contain identical genomic insert. The sequencing analysis confirmed our speculation. This 1.8kb HindIII fragment contains an open reading frame of 624 base pairs that has 64% similarity to the sequence of rat mrpe3-00078-F6-Wz. In terms of similarity in amino acid sequence, the human sequence is 40.5% identical to and 50% similar to that of rat. All 5 predicted Cysteine residues were perfectly aligned with those in rat protein sequence. Moreover, the human sequence is predicted to contain a signal peptide and cleavage site. The human IFN-like protein is strongly predicted to resemble a secreted cytokine molecule (91% probability).

**Amino Acid Sequence Alignment of Human IFN-novel,  
Rat IFN-novel and Human IFN- $\beta$**

Human IFN-novel	QOKS...I LMGIR...CTL SL...-----DCNL LNVELARVTV	36
Human IFN-beta	QKSC...A LILCH...TAL SMS...LLGV...RSSEWQCK L...L...W	43
Rat IFN-novel	QKSC...A LVAL...PIQ SQ...-----NCVY LDHTI...L	32
Consensus	Q...S...A L...I...L S...-----C...L...L...W	50
Human IFN-novel	QNLHLSSMS WSPFVECLRE NY...P...LQV...CAATYMS	86
Human IFN-beta	Q-LP...GR...-KY...CLKD HQ...P...KUL...ALTIYEM	85
Rat IFN-novel	QNLHLSSIR TTPFLRLCLO IT...P...LLV...CAVTYHS	82
Consensus	Q...P...LSS...FP...CLKD...P...LQV...CA...YMS	100
Human IFN-novel	QAPN...T PKY-WKE...-...RELKIQIG LDOQAYL	121
Human IFN-beta	NIPAL...S SSTGQMTIV EN...AVVHQ INELRTV	122
Rat IFN-novel	LALII...D SISLATE...-...ELERIRSG LFKOVQA	118
Consensus	Q...P...S...W...E...-...HLX...L...Q...	150
Human IFN-novel	CLEQDQENE DMCKCKENM KP...RVPO LSSLE...YF HRIDWFL	170
Human IFN-beta	-----LEEL EN...FQKL MSBL...YF GRLLSYL	157
Rat IFN-novel	CMVDKEN...-KVTSDST SQ...SEGPK AVYLE...YF FAIRKFLV	163
Consensus	C...EN...K...E...-...RG...SSELE...YF .RI...FLK	200
Human IFN-novel	K...R...R...TALPER K	201
Human IFN-beta	K...R...R...LTQYLAN	187
Rat IFN-novel	K...R...R...LLNGM	191
Consensus	K...R...R...LT...R	231

• Human IFN-novel is most close to human IFN- $\beta$ , with 30% identity. Four out of five cysteine residues are conserved between them.

Northern blot analysis detected IFN-like mRNA in several different stages of mouse and rat embryos. Northern blots used RNA isolated as above. The full-length rat cDNA was used as a probe. Prehyb conditions were 40 % formamide, 5X SSC, 1 mM EDTA, 0.1 % SDS, for 4 h at 42°C. Hyb conditions were the same as above except were done overnight at 42°C. Blots were washed with 0.2x SSC, 1 mM EDTA, and 0.1% SDS for 30 min at 60°C.

RT-PCR (*conditions are not necessary - standard technology*) identified IFN-like mRNA in the following human tissues : pancreas, small intestine, prostate, uterus, thyroid, and placenta.

Production of human and rat IFN-like protein in *E. coli* :

Waiting on data from Karen Sitney. However, the *E. coli* protein did not appear to be folded correctly and has not yet generated any biologically active material.



## **Production of human and rat IFN-like protein in a mammalian expression system:**

Several versions of the human and rat IFN-like protein have been produced in a mammalian expression system (either CHO or 293 cells). The proteins synthesized were either the native protein itself, or a native protein-Fc fusion. Some of the Fc fusion constructs contained a cleavage site which allows the native protein to be released from the Fc portion after being produced in the conditioned media of CHO cells.

PCR amplification of IFN-like molecule:

PCR primers were selected to amplify the coding sequence of rat/human IFN-like molecule:

### Rat IFN-Like Molecule primers:

- IFN-Like molecule Fc-fusion:

1847-77 CCC AAG CTT ACC ATG ACA CTG AAG TAT TTA TG

Forward primer: Hind III site plus ATG

1847-78 AAG GAA AAA AGC GGC CGC ATT CAT GTT GAG TAG

- Reverse primer: Not I site and no stop codon for Fc fusion

Soluble IFN-like molecule:

1896-56 ACG CGT CGA CTC ATC AAT TCA TGT TGA GTA GTT TG

Reverse primer: Sal I site plus 2 stop codons (for pDSR $\alpha$  cloning).

1896-57 AAG GAA AAA AGC GGC CGC TCA TCA ATT CAT GTT GAG TAG

Reverse primer: Not I site plus two stop codons (for pCEP4 cloning).

### Human IFN-like primers:

- Soluble human IFN-like primers:

1954-45 ACG CGT CGA CTT ATT ATT TCC TCC TGA ATA G

Reverse primer: Sal I site plus 2 stop codons (for pDSR $\alpha$  cloning).

1954-46 AAG GAA AAA AGC GGC CGC TTA TTA TTT CCT CCT GAA TAG AGC

Reverse primer: Not I site plus two stop codons (for pCEP4 cloning).

- Human IFN like-Fc fusion primers:

1955-44 CCC AAG CTT ACC ATG AGC ACC AAA CCT GAT ATG

Forward primer: Hind III site with 1st ATG

1954-47 CCC AAG CTT ACC ATG ATT CAA AAG TGT TTG TGG C

Forward primer: Hind III site with 2nd ATG

1954-48 AAG GAA AAA AGC GGC CGC GCG GCC CTC GAT TTT CCT CCT GAA TAG AGC TGT AA

Reverse primer: Not I site, no stop codon with *Factor Xa* cleavage site and Fc fusion

1954-49 AAG GAA AAA AGC GGC CGC TTT CCT CCT GAA TAG AGC TGT AA

Reverse primer: Not I site and no stop codon for Fc fusion

PCR Reaction:

### Rat:

*Reaction Mixture:* template 20 ng, 1847-77 and 1847-88 or 1896-56/57, 20 pmol each, 1mmol dNTPs, 4mM MgCl<sub>2</sub>, 1X PCR buffer, 5u Taq polymerase.

*Reaction condition:* 2 cycle-linked PCR.

94 °C for 30 sec, 50 °C for 30 sec and 72 °C for 1 minute, for a total of 4 cycles, follow by 94

°C for 30 °C sec, 55 °C for 30 sec and 72 °C for 1 minute, for a total of 26 cycles.

**Human interferon-like protein** PCR conditions:

**Reaction Mixture:** template 20 ng, 1955-44 and 1954-45 or 1954-46 (soluble form) or 1945-48/49 (Fc fusion), 20 pmol each, 1mmol dNTPs, 4mM MgCl<sub>2</sub>, 1X PCR buffer, 5u Taq polymerase.

**Reaction condition:** 2 cycle-linked PCR.

94 °C for 30 °C sec, 48 °C for 30 sec and 72 °C for 1 minute, for a total of 4 cycles, follow by 94 °C for 30 °C sec, 55 °C for 30 sec and 72 °C for 1 minute, for a total of 26 cycles.

While 1955-44 primer generates an ORF using first Met in the coding region, a separate PCR with 1954-47 to obtain an insert using 2nd downstream Met was also generated. But in terms of secretion efficiency, when tested in 293 EBNA transient transfection, there was no detectable difference could be defined.

For both rat and human, the PCR products were purified by Qiagen PCR purification spin column and subjected to restriction digestion by respective enzymes (HindIII and NotI (pCEP4) or SalI(pDSRα)). After digestion, the fragment was purified from agarose gel with Qiagen gel purification spin column. The purified fragment was quantified and ligated into pCEP4 (for native form), pCEP4-Fc (for Fc form) or pDSRα (native form or Fc form) vectors respectively. The ligation was transformed into DH10. The transformants were picked for miniprep and subsequent sequencing verification. Accuracy of each cloning fragment was verified by sequencing including the Fc junction sequence. The clone was then maxi-prepared for tissue culture transfection experiments. The IFN-Fc fragment in pCEP4-Fc vector can be released by cutting this vector with HindIII and SalI and re-ligated this fragment into pre-digested pDSRα to yield a vector suitable to transfect CHOD<sup>-</sup> cells.

**Transfection:**

- Protocol for transfection into 293 EBNA and CHO cells with lipofectin was adopted from the one used by Jin Cao. Same protocol was used to generate both transient and stable transfectants.
- A commercial available calcium phosphate transfection kit was used in CHO cell stable transfection (protocol is attached).
- A CHO cell transfection and selection protocol from Yi Luo was utilized, except calcium phosphate transfection procedure, which has a commercially available kit.

In general, lipofectin transfection yields more stable transfection colonies. Those colonies express comparable level of secreted proteins as those picked from calcium phosphate method.

**Generate conditioned media containing recombinant protein.**

In order to conduct functional studies on this interferon-like molecule, large quantity of conditioned media (CM) were generated from a pool of hygromycin selected 293 EBNA clones. The cells were cultured in Nunc Triple Flask (500cm) to 80% confluence before switching to serum free media for a week before harvesting. The CM was then sent to purification with protein A affinity chromatography. The purified protein was then used to generate a rabbit polyclonal antibody and to test for in vitro activities. The processing of signal peptide as well as partial amino acid sequence was verified by peptide sequencing.

### **Purification of human IFN-like-Fc**

Conditioned media from CHO cells expressing huIFLM-Fc was thawed and 0.2µm filtered. The filtered material was loaded onto a Protein G column that was previously equilibrated with PBS, pH 7.0. After loading, the column was washed with PBS until the absorbance at A<sub>280</sub> reached baseline. The protein was eluted from the column with 0.1M Glycine-HCl pH 2.7 and immediately neutralized with 1M Tris-HCl pH 8.5. Fractions containing huIFLM-Fc were pooled and dialyzed into PBS and stored at -70°C.

### **Factor Xa cleavage of human IFN-like-Fc**

The human IFN-like-Fc construct has a Factor Xa cleavage site (IEGR) inserted between the Fc and huIFLM. This site is cleaved with restriction protease factor Xa. The human IFN-like-Fc in PBS was dialyzed into 50mM Tris-HCl, 100mM NaCl, 2mM CaCl<sub>2</sub>, pH 8.0. The Factor Xa was added to the dialyzed protein at 1/100 (w/w). The sample was incubated overnight at room temperature.

### **Abs (available, ordered, proposed):**

#### **1. Polyclonal:**

Polyclonal antibodies were prepared using both rat and human proteins produced in E. coli and CHO cells (from above) using standard immunological techniques. Antisera were positive for the proteins as determined by Western blot analysis (standard techniques)

#### **2. Monoclonal:**

None.

#### **3. Peptides:**

None.

### **Phenotype and/or Biological Activity:**

#### **1. Transgenic /**

(pending / analyzed)

other	
<p>Because the lack of a phenotype constitutes a 'negative' result no conclusions can be drawn from this experiment. Further testing will be required to determine any or all of IFN-like proteins' biological activities in vivo.</p>	
2. <i>in vivo</i> assays:	(available, used, proposed)
<p>Not done.</p>	
3. <i>in vitro</i> assays:	(available, used, proposed)
<p>Rat IFN-like Fc fusion protein treatment of several cell lines caused phosphorylation of some cellular proteins (unidentified).</p>	

**References:**

Nothing specifically published on this gene. Lots of references for the interferon family.

**Genomic DNA Sequence (i.e. including all introns and exons):**

The human gene was cloned from genomic DNA. The attached sequence (above) comes from genomic DNA and includes the coding region which is found in one exon, and the flanking regions.

**Ortholog DNA Sequences:**

Human and rat sequences cloned.